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OM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 ; Search time 34.2312 Seconds

(without alignments)
637.949 Million cell updates/sec

Title: US-10-622-237-4

Perfect score: 2197

Sequence: 1 AAPPGLRLRLILLSAAL.....TALINAGGNNSEKKYF 423

Scoring table: BLOSUM62

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/6C.COMB.pep.*

6: /cgn2_6/ptodata/2/iaa/6D.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2197	100.0	423	4	US-09-778-510-22 Sequence 22, App1
2	2169	98.7	442	4	US-09-778-510-20 Sequence 20, App1
3	2169	98.7	442	4	US-09-930-803-1 Sequence 1, App1
4	2149	97.8	440	4	US-09-866-028-61 Sequence 61, App1
5	904	41.1	444	2	US-08-659-984A-5 Sequence 5, App1
6	904	41.1	444	3	US-08-660-531-5 Sequence 5, App1
7	893.5	40.7	421	2	US-08-658-984A-1 Sequence 1, App1
8	893.5	40.7	421	3	US-08-660-531-1 Sequence 1, App1
9	738.5	33.6	398	4	US-09-778-510-4 Sequence 4, App1
10	732.5	33.3	398	4	US-09-778-510-6 Sequence 6, App1
11	732.5	33.3	398	4	US-09-907-794A-84 Sequence 84, App1
12	732.5	33.3	398	4	US-09-905-125A-84 Sequence 84, App1
13	732.5	33.3	398	4	US-09-903-775A-84 Sequence 84, App1
14	715.5	33.6	432	4	US-09-778-510-2 Sequence 2, App1
15	333	15.2	227	4	US-09-205-258-47 Sequence 947, App1
16	252.5	11.5	517	4	US-09-723-368-4 Sequence 4, App1
17	244	11.1	518	4	US-09-915-112-20 Sequence 20, App1
18	231.5	10.5	493	1	US-08-429-742-2 Sequence 2, App1
19	226.5	10.3	479	4	US-09-723-368-2 Sequence 2, App1
20	220.5	10.0	344	4	US-09-700-397-3 Sequence 3, App1
21	216	9.8	458	4	US-09-435-956A-1 Sequence 4, App1
22	212	9.6	313	4	US-09-700-397-4 Sequence 4, App1
23	206.5	9.4	308	2	US-08-414-657D-46 Sequence 46, App1
24	206.5	9.4	325	2	US-08-414-657D-2 Sequence 2, App1
25	206.5	9.4	325	2	US-08-414-657D-41 Sequence 41, App1
26	206.5	9.4	325	2	US-09-135-080-2 Sequence 2, App1
27	206.5	9.4	338	4	US-09-976-594-404 Sequence 404, App1

28	206	9.4	388	1	US-08-429-742-4 Sequence 4, App1
29	205.5	9.4	582	4	US-09-702-705-334 Sequence 334, App1
30	205.5	9.4	582	4	US-09-736-457-334 Sequence 334, App1
31	205.5	9.4	582	4	US-09-614-124B-334 Sequence 334, App1
32	205.5	9.4	582	4	US-09-671-325-334 Sequence 334, App1
33	205.5	9.4	582	4	US-09-589-184-334 Sequence 334, App1
34	204.5	9.3	315	2	US-08-414-657D-47 Sequence 47, App1
35	204.5	9.3	338	2	US-08-414-657D-42 Sequence 42, App1
36	204.5	9.3	338	2	US-08-414-657D-43 Sequence 43, App1
37	204.5	9.3	338	4	US-09-135-080-4 Sequence 4, App1
38	204	9.3	642	1	US-08-217-299-1 Sequence 36, App1
39	204	9.3	698	2	US-08-602-725-36 Sequence 17, App1
40	204	9.3	734	2	US-08-389-459A-17 Sequence 17, App1
41	204	9.3	734	2	US-08-387-867A-17 Sequence 17, App1
42	203.5	9.3	583	2	US-08-432-016-2 Sequence 2, App1
43	203.5	9.3	583	2	US-08-684-594-2 Sequence 2, App1
44	203	9.2	1461	4	US-09-976-594-531 Sequence 531, App1
45	198.5	9.0	338	2	US-08-414-657D-60 Sequence 60, App1

ALIGNMENTS

RESULT 1

US-09-778-510-22 Application US/09778510

Sequence 22, App1

Patent No. 6512095

GENERAL INFORMATION:

APPLICANT: Baum, Peter

TITLE OF INVENTION: Molecules Designated B7L1

FILE REFERENCE: 2844-US

CURRENT APPLICATION NUMBER: US/09/778,510

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: PCT/US99/17906

PRIOR FILING DATE: 1999-08-05

PRIOR APPLICATION NUMBER: 60/095,663

PRIOR FILING DATE: 1998-08-07

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 22

LENGTH: 423

TYPE: PRT

ORGANISM: Mus musculus

US-09-778-510-22

Query Match 100.0%; Score 2197; DB 4; Length 423;

Best Local Similarity 100.0%; Pred. No. 3.6e-187; Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAPPGLRLRLILLSAALIPFGDGNLFTKVTYIEGVATISGVNKSDDSVTQLN	60
DB	1	AAPPGLRLRLILLSAALIPFGDGNLFTKVTYIEGVATISGVNKSDDSVTQLN	60
QY	61	PNRQTIIFRDFRPLKDSRFQNLNFSSELKVSITNVISIDEGRYFQLYTDPQESYTTI	120
DB	61	PNRQTIIFRDFRPLKDSRFQNLNFSSELKVSITNVISIDEGRYFQLYTDPQESYTTI	120
QY	121	TVLPPRNLMIDIOKDAVEGEIEVNCTMAKSPATTIRMFNGKELGKSVEEWSDM	180
DB	121	TVLPPRNLMIDIOKDAVEGEIEVNCTMAKSPATTIRMFNGKELGKSVEEWSDM	180
QY	181	YTTTSQMLKHKHEDDGVPIYCOVEHPAVTGNQOTRYIEVQYKPOVHIQMTYPILOGLTR	240
DB	181	YTTTSQMLKHKHEDDGVPIYCOVEHPAVTGNQOTRYIEVQYKPOVHIQMTYPILOGLTR	240
QY	241	EGDAFEITCEAIGPCQVMTWVRVDDEMPOHVLISGPNLFINNLTNGTYRCASNI	300
DB	241	EGDAFEITCEAIGPCQVMTWVRVDDEMPOHVLISGPNLFINNLTNGTYRCASNI	300
QY	301	VGKASDVMYVVDPTTPTTTTTTTTTTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVHVAIG	360
DB	301	VGKASDVMYVVDPTTPTTTTTTTTTTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVHVAIG	360

QY 361 GVAVVVFAMCLLIIIGRYFARHKGTYFTHKAGDADADADATAIINAEAGGNNSEKK 420
DB 361 GVAVVVFAMCLLIIIGRYFARHKGTYFTHKAGDADADADATAIINAEAGGNNSEKK 420
QY 421 EYF 423
DB 421 EYF 423

RESULT 2
US-09-778-510-20
Sequence 20, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 20
LENGTH: 442
TYPE: PRT
ORGANISM: Homo sapiens
US-09-778-510-20

Query Match 98.7%; Score 2169; DB 4; Length 442;
Best Local Similarity 98.8%; Pred. No. 1.2e-184;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLIIILLSAALIFPGDQNLFTKQVTVIEGEVATISQVNNKSDSVIOLN 60
DB 19 AAPPGLRLRLIIILLSAALIFPGDQNLFTKQVTVIEGEVATISQVNNKSDSVIOLN 78
QY 61 PNRQTIYFRDPRFKDSRFQNLNFSSESEKSLTVNSISDEGRYFCQLYTDPQESYTTI 120
DB 79 PNRQTIYFRDPRFKDSRFQNLNFSSESEKSLTVNSISDEGRYFCQLYTDPQESYTTI 138
QY 121 TVVPPRNLMIDIOKDTAVGEIEVNCCTAMASKPATITIRFKNGKELKSGSEVEEWSDM 180
DB 139 TVVPPRNLMIDIOKDTAVGEIEVNCCTAMASKPATITIRFKNGKELKSGSEVEEWSDM 198
QY 181 YTVTSQMLKVKHKKEDGVVICOVEHPAVTGNLQRYLEYQYKQVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHKKEDGVVICOVEHPAVTGNLQRYLEYQYKQVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIGKQPPVMTWVRVDDEMPQHAVISGPNLFINNKTDNGTYRCEASNI 300
DB 259 EGDAPFELTCEAIGKQPPVMTWVRVDDEMPQHAVISGPNLFINNKTDNGTYRCEASNI 318
QY 301 VGKASDYMLYYVDPPTTIPPTTTTTTTTTTTTTTTTTITDSRAGEEGTIGAVDHAIVG 360
DB 319 VGKASDYMLYYVDPPTTIPPTTTTTTTTTTTTTTTTTITDSRAGEEGTIGAVDHAIVG 378
QY 361 GVAVVVFAMCLLIIIGRYFARHKGTYFTHKAGDADADADATAIINAEAGGNNSEKK 420
DB 379 GVAVVVFAMCLLIIIGRYFARHKGTYFTHKAGDADADADATAIINAEAGGNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 3
US-09-930-803-1
Sequence 1, Application US/09930803
Patent No. 6596493
GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: REEVES, Roger
APPLICANT: YOSHINOBI, Mutsumaki
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILE REFERENCE: JHU1770-1
CURRENT APPLICATION NUMBER: US/09/930,803
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patent In version 3.0
SEQ ID NO 1
LENGTH: 442
TYPE: PRT
ORGANISM: Homo sapiens
US-09-930-803-1

Query Match 98.7%; Score 2169; DB 4; Length 442;
Best Local Similarity 98.8%; Pred. No. 1.2e-184;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLIIILLSAALIFPGDQNLFTKQVTVIEGEVATISQVNNKSDSVIOLN 60
DB 19 AAPPGLRLRLIIILLSAALIFPGDQNLFTKQVTVIEGEVATISQVNNKSDSVIOLN 78
QY 61 PNRQTIYFRDPRFKDSRFQNLNFSSESEKSLTVNSISDEGRYFCQLYTDPQESYTTI 120
DB 79 PNRQTIYFRDPRFKDSRFQNLNFSSESEKSLTVNSISDEGRYFCQLYTDPQESYTTI 138
QY 121 TVVPPRNLMIDIOKDTAVGEIEVNCCTAMASKPATITIRFKNGKELKSGSEVEEWSDM 180
DB 139 TVVPPRNLMIDIOKDTAVGEIEVNCCTAMASKPATITIRFKNGKELKSGSEVEEWSDM 198
QY 181 YTVTSQMLKVKHKKEDGVVICOVEHPAVTGNLQRYLEYQYKQVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHKKEDGVVICOVEHPAVTGNLQRYLEYQYKQVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIGKQPPVMTWVRVDDEMPQHAVISGPNLFINNKTDNGTYRCEASNI 300
DB 259 EGDAPFELTCEAIGKQPPVMTWVRVDDEMPQHAVISGPNLFINNKTDNGTYRCEASNI 318
QY 301 VGKASDYMLYYVDPPTTIPPTTTTTTTTTTTTTTTTTITDSRAGEEGTIGAVDHAIVG 360
DB 319 VGKASDYMLYYVDPPTTIPPTTTTTTTTTTTTTTTTTITDSRAGEEGTIGAVDHAIVG 378
QY 361 GVAVVVFAMCLLIIIGRYFARHKGTYFTHKAGDADADADATAIINAEAGGNNSEKK 420
DB 379 GVAVVVFAMCLLIIIGRYFARHKGTYFTHKAGDADADADATAIINAEAGGNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 4
US-09-866-028-61
Sequence 61, Application US/09866028
Patent No. 6642360
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Flivarov, Ellen
APPLICANT: Gerdtisen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
SEQ ID NO: 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-866-028-61

Query Match 97.8%; Score 2149; DB 4; Length 440;
Best Local Similarity 98.3%; Pred. No. 7,2e-183;
Matches 416; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 1 AAPPGLRLILLILLSAALLIPTGDSQNLFTKDVIVIEGEVATISGVNKSDDSVIQLN 60
DB 19 AAPPG--LRLILLFSAAALIPGDSQNLFTKDVIVIEGEVATISGVNKSDDSVIQLN 76
QY 61 PNRQITTFDFRPLKDSRFQNLNFSSELSKSLTNVSISSDEGRYFCQLYTDPQESYTTI 120
DB 77 PNRQITTFDFRPLKDSRFQNLNFSSELSKSLTNVSISSDEGRYFCQLYTDPQESYTTI 136
QY 121 TIVVPRNIMIDIOKTAVEGEIEVNCCTAMASKPATTTIRWFGKNEELKSGSEVERMSM 180
DB 137 TIVVPRNIMIDIOKTAVEGEIEVNCCTAMASKPATTTIRWFGKNEELKSGSEVERMSM 196
QY 181 YVTSQMLKVNHEDDGVPIYCOVEHPAVTGNLQTORYLEVOYKPCVHIQMTYPLQGLTR 240
DB 197 YVTSQMLKVNHEDDGVPIYCOVEHPAVTGNLQTORYLEVOYKPCVHIQMTYPLQGLTR 256
QY 241 EGAPFELTCALGKPOVWTTWVRVDDEMPOHNLVSGPNLFINLKTNGTYRCASNI 300
DB 257 EGAPFELTCALGKPOVWTTWVRVDDEMPOHNLVSGPNLFINLKTNGTYRCASNI 316
QY 301 VGSASDVMYVYDPTTIPPTTT 360
DB 317 VGSASDVMYVYDPTTIPPTTT 376
QY 361 GVAVAVVAVVAMCLIIILIGRYFAHKGTYFTHAKGADDAADATAIINAGGONNSEEEK 420
DB 377 GVAVAVVAVVAMCLIIILIGRYFAHKGTYFTHAKGADDAADATAIINAGGONNSEEEK 436
QY 421 EYF 423
DB 437 EYF 439

RESULT 5
US-08-659-984A-5
Sequence 5, Application US/08659984A
Patent No. 594240
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-5

Query Match 41.1%; Score 904; DB 2; Length 444;
Best Local Similarity 44.7%; Pred. No. 4,2e-72;
Matches 194; Conservative 74; Mismatches 136; Indels 30; Gaps 7;

QY 13 LLLAAA---LIPGDSQNLFTKDVIVIEGEVATISGVNKSDDSVIQLNPNRQITYFR 69
DB 17 LLLQAAASKNVKKSQGGPFLQNVIVIEGTAALTCRVNDNDVTSLOMSNPACTIYFD 76
QY 70 DFRPLKDSRFQNLNFSSELSKSLTNVSISSDEGRYFCQLYTDPQESYTTITVLPPEL 129
DB 77 DKALRDRIRIELVPSWHELSISVDVSLSDGQYCSLFTMPVKTSKAYLTVLGVDEKP 136
QY 130 MIDIOKTAVEGEIEVNCCTAMASKPATTTIRWFGKNEELKSGSEVERMS--DWTYTSQ 186
DB 137 QISGSPVPMGDMQLCTCKTSGSKPADIRFNDKEIKVKYKKEBDANKRTFTVSSST 196
QY 187 LMLKVNHEDDGVPIYCOVEHPAVTGNLQ--TORYLEVOYKPCVHIQMTYPLQGLTR 245
DB 197 LDFRVDRDSDGVAVICRVHESLNATPQVAMQVLEIHYTPSVKL---IPSTPFOEGQPL 253
QY 246 EITCEAIKPOVWTTWVRVDDEM--POHNLVSGPNLFINLKTNGTYRCASNIYVK 303
DB 254 ILTCSKSKPLPEPVLTKDGBELPDRMVVSGREINILPLNKTNGTYRCASNIYVQ 313
QY 304 AHSQVLYVYDPTTIPPTTT 349
DB 314 SAEVYLLVHVDVPTLPTTIIIPSLITVTTVTAITTSPTTSATSSIRDPNMLAGNG 373
QY 350 TIGAVDHAIVIGVAVVAVVAMCLIIILIGRYFAHKGTYFTHAKGADDAADATAIINA 409
DB 374 P---DHALIGIVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 429
QY 410 EGGONNSEEEKYF 423
DB 430 EGGONNSEEEKYF 443

RESULT 6
US-08-660-531-5
Sequence 5, Application US/08660531
Patent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-531-5

Query Match 41.1%; Score 904; DB 3; Length 444;
Best Local Similarity 44.7%; Pred. No. 4,2e-72;

Matches 194; Conservative 74; Mismatches 136; Indels 30; Gaps 7;

QY 13 LILSAANA--LITPTGGONLFTKDVTVIGEVATISCOVNSKSDSVIOLNPNROTIYR 69
DB 17 LILQAAASKNVKGSGGQFPLONTVVEGTAHILTCRVQDNDNTSLQWSPAQOTLTFD 76
QY 70 DRRPLKDSRFPOLINSSSELKVSILNVSISDEGRYFCOLYDPPQESYTTITVLPENL 129
DB 77 DKALRDNRILVRAWSMELISVSDVSLSDGQYCSLFTVPVTKSAVLTGVPKXP 136
QY 130 MIDIOQDVAEGEELEVNCTAMASKPATIRFKNKELKGSVEEMS---DWTYVTSQ 186
DB 137 QISGESSVMEGDLNQLTKTSGSKPADIRFKNDKEIKDYKYLKEEDANKRTFTVST 196
QY 187 LMLKVKHEDDGVFVTCQVHPAVTGNLQ--TORYLEVOYKPOVNIQMTYPLQGLTREGDAF 245
DB 197 LDFRVDRSDGVAVICRVVHESLNATPQVAMQVLEIHYPVKI---IPSTPFQEGGPL 253
QY 246 ELTCEALIGKPOVMTWVRVDEM--POHAYLSGNLFINNLKNDNGTYRCEASNIYVK 303
DB 254 ILTCSKSGPLPEPLMTKDGELDPDRMVSSGELNLLINKNDNGTYRCEATNTIGQ 313
QY 304 AHSQVNLVYDDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 349
DB 314 SAAEVLIVHDVPTNLLPTTIIIPSLTAVTTVAITTSPTTSATTSIRDPNLAQNG 373
QY 350 TIGAVDAVATGVAVVVPVPAULCLIIIGRFARHKGYFTHEAKGADADAADTAIINA 409
DB 374 P---DHALIGIVAVVVFVTLCSIFLLGRYLARKKGYLTNTEAKGADADADTAIINA 429
QY 410 EGGQNNSEKKEKF 423
DB 430 EGSQVNAEKEKF 443

RESULT 7
US-08-659-984A-1
; Sequence 1, Application US/0865984A

Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sima, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-1

Query Match 40.7%; Score 893.5; DB 2; Length 421;
Best Local Similarity 45.0%; Pred. No. 3.3e-71;
Matches 188; Conservative 73; Mismatches 130; Indels 27; Gaps 6;

QY 26 GQNLFTKDVTVIGEVATISCOVNSKSDSVIOLNPNROTIYRDPRLKDSRFPOLNFS 85
DB 10 GQFPLQNTVVEGTAHILTCRVQDNDNTSLQWSPAQOTLTFDQKALRDNRILVRA 69
QY 86 SSELKVSILNVSISDEGRYFCOLYDPPQESYTTITVLPENLMIDIOQDVAEGEELE 145
DB 70 WHELSISVSDVSLSDGQYCSLFTVPVTKSAVLTGVPKPOISGESSVMEGDLNQ 129
QY 146 VNCTAMASKPATIRFKNKELKGSVEEMS---DWTYVTSQMLKVKHEDDGVFVTC 202
DB 130 LTKTSGSKPADIRFKNDKEIKDYKYLKEEDANKRTFTVSTLDFRVDRSDGVAVIC 189
QY 203 QVHPAVTGNLQ--TORYLEVOYKPOVNIQMTYPLQGLTREGDAFELTCEALIGKPO 261
DB 190 RVHESLNATPQVAMQVLEIHYPVKI---IPSTPFQEGGPLILTCSKSGPLPEPLV 246
QY 262 WVRVDEM--POHAYLSGNLFINNLKNDNGTYRCEASNIYKRAHSDVNLVYDDPTT 319
DB 247 WTKDGELDPDRMVSSGELNLLINKNDNGTYRCEATNTIGQSSAAEVLIVHDVPTN 306
QY 320 PPTTT 365
DB 307 LPTTIIIPSLTAVTTVAITTSPTTSATTSIRDPNLAQNGP---DHALIGIVAV 362
QY 366 VVPVPAULCLIIIGRFARHKGYFTHEAKGADADAADTAIINAGQNNSEKKEKF 423

Db 363 VFVTLCSIFLLGRYLARKHGYLTNEAKGADPADADTAIINAEQVNAEKEKEF 420

RESULT 8

US-08-660-531-1
 ; Sequence 1, Application US/08660531
 ; Patent No. 6221645
 ; GENERAL INFORMATION:
 ; APPLICANT: Chrysler, Susanna M.S.
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Keim, Pamela S.
 ; APPLICANT: Anderson, John P.
 ; TITLE OF INVENTION: Beta-Secretase
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Ctr., 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/660,531
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/480,498
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heeslin, James M.
 ; REGISTRATION NUMBER: 29,541
 ; REFERENCE/DOCKET NUMBER: 15270-002210US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 421 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-660-531-1

Query Match 40.7%; Score 893.5; DB 3; Length 421;
 Best Local Similarity 45.0%; Pred. No. 3.3e-71;
 Matches 188; Conservative 73; Mismatches 130; Indels 27; Gaps 6;

QY 26 GQNLFTKDVTVIEGEVATISCOVNSDDSVIQLNPNRQTIYRDRPKDSRFPOLLNS 85
 DB 10 GGPPLQNTVYVGGVAILTCRDQNDNTSLQMSNPACQTLFYDDKALRDRRIELVPA 69
 QY 86 SSELKSLTNVSDSGRYFCOLYTPPOESYTTITLVPRNNIMIDIOKDAVEGEIE 145
 DB 70 WHLELSVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKPOLSGSSSVMGDLMO 129
 QY 146 VNCSTAMASRPATTIRFNKNGKELKGSVEVEMS--DNYTTSQMLKVNKEDGVPIYC 202
 DB 130 LICKTSKSPADIRFKNKDKIKDVYKLEEDANRKTFTVSGTLDPRVRSDDGVAIYC 189
 QY 203 QVEHPAVTNLQ--TQVLEVOYKQVHIQMTYPLGLTREBDAFELTCEALIGKRPVWT 261
 DB 190 RVDHESLNTPOVAMOVLEIHTPSVKI--IPSTPFQEGPLILITGSKGKPLBEPVL 246
 QY 262 WVRVDDM--PQHAVLSGNLFLNNLKNKTNGTYRCEASNIYGAKASHDYMLVYDPPPTI 319
 DB 247 WTKDGELEPDPDRMVVSGRELNLFLNKTNDNGTYRCEATNTIGSSAEVLLVHDVPNTL 306

QY 320 PPTTTTTTTTTTTTTTTTTT-----DSRAGEESTIGAVDHAVIGVAV 365
 DB 307 LPTTIISLTATVTTVAITTSPTTSATTSIRDPNALGQNP-----DHALLGGLVAV 362
 QY 366 VFVPMCLLITIGYFPAHKGTYTTHAKGADDAADTAIINAEQVNAEKEKEF 423
 DB 363 VFVTLCSIFLLGRYLARKHGYLTNEAKGADPADADTAIINAEQVNAEKEKEF 420

RESULT 9

US-09-778-510-4
 ; Sequence 4, Application US/09778510
 ; Patent No. 6512095
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter
 ; TITLE OF INVENTION: Molecules Designated B7L1
 ; FILE REFERENCE: 2844-US
 ; CURRENT APPLICATION NUMBER: US/09/778,510
 ; PRIOR FILING DATE: 2001-02-07
 ; PRIOR APPLICATION NUMBER: PCT/US99/17906
 ; PRIOR FILING DATE: 1999-08-05
 ; PRIOR APPLICATION NUMBER: 60/095,663
 ; PRIOR FILING DATE: 1998-08-07
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 398
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-778-510-4

Query Match 33.6%; Score 738.5; DB 4; Length 398;
 Best Local Similarity 38.8%; Pred. No. 1.9e-57;
 Matches 165; Conservative 73; Mismatches 136; Indels 51; Gaps 9;

QY 12 LLLLSAALIPYTG-----DQNLFTKDVTVIEGEVATISCOVNSDDSVIQLNPNRQTI 66
 DB 11 LLLLLASMAFGANLSQDSDSPWTSDETVAAGTVLKQVNDHESSIQMSNPACQTL 70
 QY 67 YFRDPRPKDSRFPOLLNFSSELKSLTNVSDSGRYFCOLYTPPOESYTTITLVPR 126
 DB 71 YFGKRALRDRRIQVSTHSLISISNVALADEGEGYCSIFMPVRIKSLVTVLGI 130
 QY 127 RNLMIDIOKDAVEGEIEVNCCTAMASKPATTTIRMFKNKELG-KSEVEMSD--NYTV 183
 DB 131 QPILITGKSLRKETATLNCSSGSKPAQQLTRKGDQLHDDQRTIODEPYKTFIV 190
 QY 184 TSQMLKVNKEDDGPVICOVHPAVTG-NLQTORYLEVOYKQVHIQMTYPLGLTRREG 242
 DB 191 SSSVSFQVTRDDGAINVCSVNHESLKGADRSQREVLVYTPAMIR---PEPAHREG 247
 QY 243 DAFELTCEALIGKRPVAVTVVRVDDM--QHAVLSGNLFLNNLKNKTNDNGTYRCEAS 298
 DB 248 QKLLHCEGSGNPVQVYVWVKGSEPPKMTQESALIFP---FLNKSDSGYTGCTAT 302
 QY 299 NIVGKASHDYMLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTITINDSRAGESTIGAVNHAV 358
 DB 303 SNMGSTAYVFLTNNDSS---PVSSSSSTV-----HAI 332
 QY 359 IGVVAVVPMALCLLILIGYFPAHKGTYTTHAKGADDAADTAIINAEQVNAEKEKEF 418
 DB 333 IGGIVAFIVPLILILIFLGHYLRHKGTYLTHAKGSDPADADTAIINAEQVNSGDD 392
 QY 419 KKEYF 423
 DB 393 KKEYF 397

RESULT 10
 US-09-778-510-6
 ; Sequence 6, Application US/09778510
 ; Patent No. 6512095
 ; GENERAL INFORMATION:

APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 1999-06/095,663
PRIOR FILING DATE: 1999-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 6
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapien
US-09-778-510-6

Query Match 33.3%; Score 732.5; DB 4; Length 398;
Best Local Similarity 38.3%; Pred. No. 6,5e-57;
Matches 162; Conservative 74; Mismatches 144; Indels 43; Gaps 8;

QY 10 LLLLLLSAALIPFG-----DQNLFTKDVYIEGEVATISGVNKKSDSVIQLNPNRQ 64
DB 9 LLLLLLFACCWAPGAGNLSQDDSQPWTSDETVVAAGTVVLKQVNDHEDSSLOWSNPAQ 68
QY 65 TIYFRDPRFKDSRFOLNFSSELKVSILTNVISDEGRYFCQLYTDPQESYTTITVLV 124
DB 69 TIYFGEKALRDNRQLVSTPHELSISNVALADEGEYTCIFTPVTRAKSLVTVLG 128
QY 125 PRNLIMIDIQDVAEGEIEVNCCTAMASKPATTTIRWKNELKKG-SEVEWSD--MY 181
DB 129 IPQKPIITGKSLREKDTATLNCSSGSKPAARLWTRKGOEHLGEPTRIOEDPNKTF 188
QY 182 TVTSOLMKVHKEDGVPIQVEHPAVTG-NLQTRKLEYQKQVHIOQVTFPQGLTR 240
DB 189 TVSSSVTTQVTRVEDDCASTVCVNHESLKGADRSISQILEVLYPTAMIRDP--HPR 245
QY 241 ESDAEELTCEALGKQPVWTVWRVDEMPOHVAVLGNNLFINNKTDNGTYCEASNT 300
DB 246 ECGKLLHCEGRGNFVPCQYLWEK-EGSVPLKMTQESALIFPPLNKSDSGTYCTATSN 304
QY 301 VGRKASDVMLYYDDPTTTPPTTTTTTTTTTTTTTTTTTTTTLIIIDSRAGEGTTGADVHAIVG 360
DB 305 MCSYKAYVTLNVDNS--PVPSSSTY-----HALIG 334
QY 361 GVAVAVVPMCLLILIGRYFARHKGTYFTHEKAGDADAADTAIIINAEGQNNSEBK 420
DB 335 GIVAFIVFLILMLIFLGHYLLRHKGTYLTHAKGSDADPADDTALINAEQGSGGDDKX 394
QY 421 EYF 423
DB 395 EYF 397

RESULT 11
US-09-907-794A-84
Sequence 84, Application US/09907794A
Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Auefin L.
APPLICANT: Hillen, Kenneth, J.
APPLICANT: Kijavlin, Ivar U.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO: 84
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-794A-84

Query Match 33.3%; Score 732.5; DB 4; Length 398;
Best Local Similarity 38.3%; Pred. No. 6,5e-57;
Matches 162; Conservative 74; Mismatches 144; Indels 43; Gaps 8;

QY 10 LLLLLLSAALIPFG-----DQNLFTKDVYIEGEVATISGVNKKSDSVIQLNPNRQ 64
DB 9 LLLLLLFACCWAPGAGNLSQDDSQPWTSDETVVAAGTVVLKQVNDHEDSSLOWSNPAQ 68
QY 65 TIYFRDPRFKDSRFOLNFSSELKVSILTNVISDEGRYFCQLYTDPQESYTTITVLV 124
DB 69 TIYFGEKALRDNRQLVSTPHELSISNVALADEGEYTCIFTPVTRAKSLVTVLG 128
QY 125 PRNLIMIDIQDVAEGEIEVNCCTAMASKPATTTIRWKNELKKG-SEVEWSD--MY 181
DB 129 IPQKPIITGKSLREKDTATLNCSSGSKPAARLWTRKGOEHLGEPTRIOEDPNKTF 188


```

APPLICANT: Ford, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlsten, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-08-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-775A-84

Query Match      33.3%; Score 732.5; DB 4; Length 398;
Best Local Similarity 38.3%; Pred. No. 6.5e-57;
Matches 162; Conservative 74; Mismatches 144; Indels 43; Gaps 8;

QY      10 LLLLLISAAALPTG-----DGNLFTKVTYVIEGEVATISQVVKSDSVYQLINPRK 64
DB      9 LLLLLIFACCMAPGAGNISQDDSQPWTSETVAGTVLAKQVXDHESSIQWSPAQ 68
QY      65 TTYFRDFRLKDSRFQNLNFSSELKVLTNVISIDEGRYFQLYTDPPQESYTTITIV 124

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DB      69 TLYFGKRALRDNRLQLVSTPHEHSISISNVALDEGGYTSITMPRTAKSLVTVIG 128
QY      125 PPRNLMDIQDXTAVEGEIEIVNCTAMASKPATITRMFGKNELKGR--SEVEWSD--MY 181
DB      129 IPQKPIITGVKSLRKKDITAINLQSSGSKPAPARLTKRGDGLGEPFRIGEDPNGKTF 188
QY      182 TTTSQLMKVKNHEDDGVPIQVEHPAYTG--NLQTRVIEVQYKXQVHQMTPYIQLGLTR 240
DB      189 TVSSSVTFQYTRDDASIVCSVNHESLKGARSTQRLEVIYTPAMIRDPF--HPR 245
QY      241 EGDAPFELTCEAIGKPPQVWVTVWRVDEMPQHAIVSGPULFINNKTNDNGTYRCEASNI 300
DB      246 EGQKLLHCEGRNPPQOYLMEK--EGSVPLKMQESALLPPLNKSDSGTGTATSN 304
QY      301 VGRASDYNLYVYDPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 360
DB      305 MGSYKAYTLNVNDPS---FVPSSESTY-----HALLG 334
QY      361 GVVAVVVPAMLCLLITIGYFAPRHKQYFTEAKGADADADATAIINAGSQNNSEERK 420
DB      335 GIYAFIVFLMLMLILGHYLRHKQYLTTHAKGSDAPADDTAIINAGSQSGDDGX 394
QY      421 EYF 423
DB      395 EYF 397

RESULT 14
US-09-778-510-2
Sequence 2, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 432
TYPE: PRT
ORGANISM: Homo sapien
US-09-778-510-2

Query Match      32.6%; Score 715.5; DB 4; Length 432;
Best Local Similarity 36.1%; Pred. No. 2.4e-55;
Matches 165; Conservative 75; Mismatches 140; Indels 77; Gaps 10;

QY      10 LLLLLISAAALPTG-----DGNLFTKVTYVIEGEVATISQVVKSDSVYQLINPRK 30
DB      9 LLLLLIFACCMAPGAGNISQDDSQPWTSETVAGTVLAKQVXDHESSIQWSPAQ 68
QY      31 TKDVTYIEGEVATISQVVKSDSVYQLINPRKQITTFPDLKDSRFQNLNFSSELK 90
DB      69 TSDETVAGTVLAKQVXDHESSIQWSPAQQITLYFGKRALRDNRLQLVSTPHEHS 128
QY      91 VSLTNVISIDEGRYFQQLYTDPPQESYTTITIVLPPRNLMDIQDXTAVEGEIEVNCTA 150
DB      129 IISNVALDEGGYTSITMPRTAKSLVTVLGIQKPIITGVKSLRKKDITAINLQSS 188
QY      151 MASKPATITRMFGKNELKGR--SEVEWSD--MYTTSQMLMKVKNHEDDGVPIQVEHP 207
DB      189 SGSKPAPARLTKRGDGLGEPFRIGEDPNGKTFVSSVTFQYTRDDASIVCSVNH 248
QY      208 AVTG--NLQTRVIEVQYKXQVHQMTPYIQLGLTRVEDAEVLCEALGKQPPWTVWRVD 266
DB      249 SLKGDARSTQRLEVIYTPAMIRDPF--HPRGQKLLHCEGRNPPQOYLMEK--E 304

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QY 267 DEWPQAVUSGPNLFINNLTNDNGTYRCEASNIYKAHSDMYLYVDEPTTTPPTTT 326
DB 305 GSVPLKMTQESALIPFPFNKSDSGTYCTATSNMGSYKAYTTLNVNPS--PVPSSSS 361
QY 327 TTTTTLTTLTITDSRAGEGTIGAVDHAVIGVAVVAVPAMCLITILGRYFARKHG 386
DB 362 TV-----HAIIGGVAIVLVLMLIFLGHYLRHKG 394
QY 387 TYTFHEAKADDAADDTAIINAEGGNNSEKKEYF 423
DB 395 TYLTHEAKGSDPADDTAIINAEGGSGDDKKEYF 431
RESULT 15
US-09-205-258-947
Sequence 947, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,992
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 947
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-947
Query Match 15.2% Score 333 DB 4 Length 227
Best Local Similarity 33.3% Pred No. 9.8e-22
Matches 77; Conservative 49; Mismatches 97; Indels 8; Gaps 5;
QY 88 ELKYSLTNVSISDEGRYFCQLYTDPQESYTTITVLPNNLMIDIKDTAVAGEELEVN 147
DB 1 ELSISINVALADGEYTCISFTVPVTAKSILTVLGIPOKPIITGVKSLREXDGTATLN 60
QY 148 CTMAASKPATTIIPFNKNNKELKXK-SEVEEMSD--MYTVSQMLKYNKREDDGVPIYCOV 204
DB 61 CQSSGSRPARLTIWRKQDQELHGFRTIQDPPGKTFVSSSVTFQVTRDDGASIVCSV 120
QY 205 EHPAVTG-NLQTCRYLEVQYKPVNIQMTYPLQGLTEGDAFELTCAIGKPOPVVWTWV 263
DB 121 NHESLKGADSTSGRIIVLVTPTAMIRPDP--HPEEGKLLHCGRGNPVPOQYLWE 177
QY 264 RVDEMPQHAVLSGPNLFINNLTNDNGTYRCEASNIYKAHSDMYLYVDEPTTTPPTTT 314
DB 178 K-EGSVPLKMTQESALIPFPFNKSDSGTYCTATSNMGSYKAYTTLNVNPS 227

Search completed: July 7, 2004, 06:05:19
Job time : 35.2312 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 ; Search time 33.7249 Seconds
(without alignments)
1260.692 Million cell updates/sec

Title: US-10-622-237-2

Perfect score: 2283

Sequence: 1 MASVLPFSGSCCAAAAAA.....AIIAAGGQNNSEKKEYFI 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	268	11.7	407	2 T08732	hypothetical prote
2	263.5	11.5	5175	2 T20992	hypothetical prote
3	263.5	11.5	5198	2 T43290	hemectin precurs
4	248	10.9	518	2 JC4024	poliovirus recepto
5	247.5	10.8	530	2 A53437	poliovirus recepto
6	244	10.7	417	2 A44194	poliovirus recepto
7	244	10.7	467	1 HIMS93	poliovirus recepto
8	243	10.6	725	2 JE0099	neural cell adhesi
9	242.5	10.6	538	2 I68093	PRR2 delta - human
10	241.5	10.5	392	2 B44194	poliovirus recepto
11	240	10.5	392	1 RMHUPD	poliovirus recepto
12	240	10.5	417	1 RMHUPA	poliovirus recepto
13	239	10.5	1088	1 IJXLNL	neural cell adhesi
14	230.5	10.1	4162	2 T42633	connectin/citin -
15	230	10.1	344	2 I56551	neurotrophin - rat
16	226	9.9	812	2 B42632	cell adhesion mole
17	226	9.9	932	2 A42632	cell adhesion mole
18	225	9.9	7962	2 I38346	elastic titin - hu
19	223.5	9.8	1011	2 T13669	neuromusculin - fr
20	223	9.8	725	2 JE0100	neural cell adhesi
21	223	9.8	1092	1 JN0635	neural cell adhesi
22	222	9.7	478	2 I53960	PRR2 alpha - human
23	218.5	9.6	345	2 S03199	opioid-binding pro
24	218.5	9.6	588	2 A45254	surface glycoprote
25	217	9.5	588	2 JH0506	adhesion molecule
26	216.5	9.5	345	2 JC4025	opioid-binding cel
27	216	9.5	765	2 C42632	cell adhesion mole
28	214	9.4	4391	2 A38096	perlecan precursor
29	210.5	9.2	345	2 JC1239	opioid-binding pro

30	209.5	9.2	584	2 I50419	s-glycerin precursor
31	209	9.2	336	2 JCS519	50K glycoprotein p
32	206	9.0	702	2 A56319	carcinoembryonic a
33	205.5	9.0	338	2 JC4776	limbic-system-asso
34	205.5	9.0	646	2 I38049	cell surface glyco
35	204.5	9.0	338	2 JC1238	opioid-binding pro
36	204	8.9	3707	2 S18252	heparan sulfate pr
37	203	8.9	1323	2 P00568	connectin 3B - chi
38	202.5	8.9	862	2 I49583	differentiation an
39	202.5	8.9	868	2 A46512	CD22 homolog/B 1ym
40	202	8.8	847	2 JH0371	B-cell adhesion pr
41	202	8.8	1443	2 I50600	neogenin - chicken
42	199.5	8.7	1241	2 T37190	nephrin - human
43	197	8.6	583	2 I39428	alcam - human
44	196	8.6	1091	1 IJCXNL	neural cell adhesi
45	195.5	8.6	1612	2 T30805	ductal protein - mo

ALIGNMENTS

RESULT 1
T08732
Hypothetical protein DKFZps56B0846.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C/Accession: T08732
R/Ottensmeyer, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A/Reference number: Z16474
A/Accession: T08732
A/Molecule type: mRNA
A/Residues: 1-407 <OT>
A/Cross-references: EMBL:AL050071
A/Experimental source: fetal kidney; clone DKFZps56B0846
C/Genetics:
A/Note: DKFZps56B0846.1

Query Match 11.7%; Score 268; DB 2; Length 407;
Best Local Similarity 26.7%; Pred.No. 1.4e-11;
Matches 84; Conservative 60; Mismatches 123; Indels 48; Gaps 13;

QY	120	GRYFCQLYDP--PQESVTTITVLPFRNLMIDQKOTAVBG--EEEVNCTAMASRPAT 175
DB	2	GKTYCKAVTFPLGNAQSSITVTVLVEPTVSLIK-GPDSLIDGNETVAACIATGKPPVA 60
QY	176	TIRPFKNTLKGSEVEWSDMY-----TTSQMLKHKEDDGVPTCQVEHPAVTGN 230
DB	61	HIDW-EGDL-----GEMESTTSPFNEMATIIISQYKLPTRFARGRIITCVKHPALEKD 114
QY	231	LQTORYLEVOYKPPQVYHQMTPYPLQGLTRGDALFLTEALGKPPQPVVTVWRVDENPQH 290
DB	115	IRYFILDIDQAPBVSATYGVDMFVGKRG--VNLKCNADANPFPKSVSRDLGQWPDG 172
QY	291	AVLGGPNL-FNNNKTNDNGTYRCEASNIYKASDNLVYVDP--TTIP-----PTT 342
DB	173	LLAADNLTHTFVHPLTFVWSGVYICKVNSLQGRSDQVYIISDPPTTTTIOPTIQMPST 232
QY	343	TTTTTTTT-----TTTITITTSRAGEBGSIRAVDAVIGVAVVVFAMLCILT- 393
DB	233	ADIEDLATPEPKLPFPLSTIATI-----KDTIATIIASVVGALFIVLVSIAIFC 265
QY	394	-----ILGRYFARH 402
DB	286	YRRRTTRGDIYFAKN 300
RESULT 2		
T20992		
Hypothetical protein F1569.4a - Caenorhabditis elegans		
C/Species: Caenorhabditis elegans		
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000		
C/Accession: T20992; T24733		

R/Sulston, J.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: Z19355
 A:Accession: T20992
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5175 <MT>
 A:Cross-references: EMBL:Z47068, PIDN:CAA87335.1, GSPDB:GN00028, CESP:F15G9.4a
 A:Experimental source: clone F15G9
 R/Kershaw, J.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: Z19929
 A:Accession: T24733
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5175 <MT>
 A:Cross-references: EMBL:Z47070, PIDN:CAA87344.1, GSPDB:GN00028, CESP:F15G9.4a
 A:Experimental source: clone T09B9
 C/Genetics:
 A:Gene: CESP:F15G9.4a
 A:Map position: X
 A:Introns: 85/1, 120/1, 334/3, 370/1, 477/2, 606/3, 664/1, 935/3, 977/1, 1051/3, 1184/3;
 2512/2; 2593/3; 2699/3; 2759/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
 1, 4225/1, 4361/1, 4408/1, 4456/1, 4498/1, 4647/3, 4838/1, 4879/1, 4941/1, 5011/1, 5077/1

Query Match 11.5%; Score 263.5; DB 2; Length 5175;
 Best Local Similarity 24.6%; Pred. No. 7, 6e-10;
 Matches 87; Conservative 66; Mismatches 129; Indels 71; Gaps 15;

QY 52 VTVIEGEVATISQVKNKSDSVIQLNPNRQTYPRDFPPL---KDSRFQLNBSSEL 107
 DB 2200 VTAIKGALPFCPID--DDK-----NFKQIIMLNHYQPIDLEADDAITRL---SND 2249
 QY 108 KVALTNVTSIDEGRYFCQLYTDPPOSYT-TITVLPNPNLMIDIQD-TAVEGEIEVN 165
 DB 2250 RLTLTNTEDEQYSCRKNDAGENSFPKATVLPPIITIMDKDKNTAHEHSVTLS 2309
 QY 166 CTAMASKPATITRMFKG-----NTELKSKSEVEWSDMYTTSQMLKVKH 211
 DB 2310 CPA-TGKRPBDITWFKDGEAIIHENTADIIPNGLNG-----NQLKITRIK 2354
 QY 212 EDGCVPIQCVHEPATYGNLQTORYLEVOYKPOVH---IQMYPLQGLREGDALELCE 268
 DB 2355 EGAGKTYTCADNSA--GSVEQDVNNAVITTPKIEKDGIPSDIESQ---QNERVVISCP 2408
 QY 269 AIGKPCPVMTWYRVDDMPQHAVL-----SGPNLFINNINKTNGYRCEASNIYKAKHS 324
 DB 2409 VYARP-PAKITWIKAGKPLQSDKFKVTSANGQLYFKLRETDSSKYTCIATNEAGTDKR 2467
 QY 325 DYNLYVYDPTTTP-----PTTTTITTTTTITITITDSRAGE 365
 DB 2468 DFKVSMLVAPSFDEPNIVRITVNSGNPSTLHCAPAKGSPSTITWLDGNALIE 2520

RESULT 3
 T43290
 hemiscentin precursor - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
 C/Accession: T43290; T20993; T24734
 R/Vogel, B.E.; Hedgecock, E.M.
 submitted to the EMBL Data Library, June 1998
 A:Description: Hemiscentin is required for hemidesmosome mediated cell adhesion and germ-
 A:Reference number: Z22396
 A:Accession: T43290
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-5198 <VOG>
 A:Cross-references: EMBL:AF074901; PIDN:AAC26792.1
 R/Sulston, J.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: Z19355
 A:Accession: T20993

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5198 <MT>
 A:Cross-references: EMBL:Z47068, PIDN:CAA87336.1, GSPDB:GN00028; CESP:F15G9.4b
 A:Experimental source: clone F15G9
 R/Kershaw, J.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: Z19929
 A:Accession: T24734
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5198 <MT>
 A:Cross-references: EMBL:Z47070, PIDN:CAA87345.1, GSPDB:GN00028; CESP:F15G9.4b
 A:Experimental source: clone T09B9
 C/Genetics:
 A:Gene: h1n-4; F15G9.4b
 A:Map position: X
 A:Introns: 85/1, 120/1, 334/3, 370/1, 477/2, 606/3, 664/1, 935/3, 977/1, 1051/3, 1184/3;
 2512/2; 2593/3; 2699/3; 2759/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
 1, 4225/1, 4361/1, 4408/1, 4456/1, 4498/1, 4647/3, 4838/1, 4902/1, 4964/1, 5034/1, 5100/1

Query Match 11.5%; Score 263.5; DB 2; Length 5198;
 Best Local Similarity 24.6%; Pred. No. 7, 6e-10;
 Matches 87; Conservative 66; Mismatches 129; Indels 71; Gaps 15;

QY 52 VTVIEGEVATISQVKNKSDSVIQLNPNRQTYPRDFPPL---KDSRFQLNBSSEL 107
 DB 2200 VTAIKGALPFCPID--DDK-----NFKQIIMLNHYQPIDLEADDAITRL---SND 2249
 QY 108 KVALTNVTSIDEGRYFCQLYTDPPOSYT-TITVLPNPNLMIDIQD-TAVEGEIEVN 165
 DB 2250 RLTLTNTEDEQYSCRKNDAGENSFPKATVLPPIITIMDKDKNTAHEHSVTLS 2309
 QY 166 CTAMASKPATITRMFKG-----NTELKSKSEVEWSDMYTTSQMLKVKH 211
 DB 2310 CPA-TGKRPBDITWFKDGEAIIHENTADIIPNGLNG-----NQLKITRIK 2354
 QY 212 EDGCVPIQCVHEPATYGNLQTORYLEVOYKPOVH---IQMYPLQGLREGDALELCE 268
 DB 2355 EGAGKTYTCADNSA--GSVEQDVNNAVITTPKIEKDGIPSDIESQ---QNERVVISCP 2408
 QY 269 AIGKPCPVMTWYRVDDMPQHAVL-----SGPNLFINNINKTNGYRCEASNIYKAKHS 324
 DB 2409 VYARP-PAKITWIKAGKPLQSDKFKVTSANGQLYFKLRETDSSKYTCIATNEAGTDKR 2467
 QY 325 DYNLYVYDPTTTP-----PTTTTITTTTTITITITDSRAGE 365
 DB 2468 DFKVSMLVAPSFDEPNIVRITVNSGNPSTLHCAPAKGSPSTITWLDGNALIE 2520

RESULT 4
 JC4024
 poliovirus receptor-related protein precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
 C/Accession: JC4024
 R/Lopez, M.; Bherle, F.; Mattei, M.G.; Gabert, J.; Bitz, F.; Bardin, F.; Maroc, C.; Dubr
 Gene 155, 261-265, 1995
 A>Title: Complementary DNA characterization and chromosomal localization of a human gene
 A:Reference number: JC4024; M01D:95237621; PMID:7721102
 A:Accession: JC4024
 A:Molecule type: mRNA
 A:Residues: 1-518 <LOP>
 A:Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
 C/Genetics:
 A:Gene: GDB:PVARI
 A:Cross-references: GDB:583951
 A:Map position: 11q23-11q24
 C/Superfamily: poliovirus receptor; immunoglobulin homology
 C/Keywords: glycoprotein; transmembrane protein
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
 F:356-379/Domain: transmembrane #status predicted <TM>

F,36,72,82,139,287,308,333/Binding site: carbohydrate (Aan) (covalent) #status predicted

```
Query Match      10.9%; Score 248; DB 2; Length 518;
Best Local Similarity 25.4%; Pred. No. 4.9e-10;
Matches 105; Conservative 60; Mismatches 154; Indels 94; Gaps 20;

QY 74 IQLNPRQTIYFDFRPLKDSRFOLNPFSSSEIKVLTNWSISDEGRYFCQYTPDP--131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 78 VAINPMGVSVALAPR-----ERVEFLRPSTPTOTILSLLEDEBQVYICERATPTG 133

QY 132 QESTITTLVPPRNLMIDIQD-TAVEGEIEV--NCTAMASKPATITRMKGNTEK 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 134 RESQNLNTLVAKPTNMLEGTQAVLPAKKQDDKVLVATCTSAANGKPSVSW--ETRLK 190

QY 188 GKSEV--EEMSDM--YVTSQMLMKVAKEDDGVVLCQVHPAVTGNLTQRY-----LE 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 191 GEAVVPGDSTPMAPVTVISRYLVPSREAHQSLACTV-----NYHMDRESLITLN 243

QY 239 VOYKPOVHIQ--MTYPLQGLTRGDALLETCEAIKRPQVMTVAVDEMPQAHVLSG 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 244 VOYEPEVTLIGFDGNWYLQRMW----VKLTCKADANPRAVEYHMTLNSLKGVAQW 298

QY 296 PNLFINN-LNKDNGTCRCASNIYGAHSDYMLVYDPTTTPPTTTTTTTTTTTTT 354
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 299 RLPFKGPINYSLAGYICENATPIGRSGQVEVNTIEFPYTSPE-----345

QY 355 LTIITDSRAGEEGSIRAVDHAIVGVAVVAVFAMLCILILIGRYFA----RH--KGYFT 408
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 346 ----HGRRAQ-----FVPTALLIGVAGSI---LVLIVIGVGLVALRRRHFKPDYR 392

QY 409 -----HEAKGA-----DDAADDTIINABGGQNNSEKKE 439
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 393 KHAVYNGYSKAGIPQHHPMAQNLQYDDSDDEKKA--GPLGSSSYEEEEE 443
```

RESULT 5

A53437
poliovirus receptor mPVR - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C/Accession: A53437
R/Koike, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8438, 1994
A/Title: Amino acid residues on human poliovirus receptor involved in interaction with F
A/Reference number: A53437; MUID:94119228; PMID:8132569
A/Accession: A53437
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-530 <AOK>
A/Cross-references: GB:D26107; NID:9475017; PIDN:BA05103.1; PID:9825507
A/Experimental source: C57/BL6, brain
A/Note: Sequence extracted from NCBI backbone (NCBIN:146664, NCBI:P:146667)
C/Superfamily: poliovirus receptor; immunoglobulin homology
F,47-133/Domain: immunoglobulin homology <IMM>

Query Match 10.8%; Score 247.5; DB 2; Length 530;
Best Local Similarity 22.1%; Pred. No. 5.5e-10;
Matches 91; Conservative 63; Mismatches 166; Indels 91; Gaps 14;

```
QY 15 AAAAAADPG-----LRLRLLLLFSAALIPDGDQNLFTKDYVIEGEV--ATISQCV 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2  ARAAVLPSPSLSPFLPLPLLL-----LLETGAQVAVRVLPVAVGRGLGTVLEPCHL 56

QY 67 -----NKSDSVIQLNPNKQTIYFRDPRPLDSRFQJ-----LNPSSS 105
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 57 LPPPTTGVQVWQRLDGLVAAAFHS-----FGVDENSOFSKORLSFVAREPETAADR 112

QY 106 ELKVLTNVVISDEGRYFCQYTPD--PQSYTTITLVPPRNLMIDIQDITAVEGEIE 163
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 113 DATLAFGLRVEDENGTCEPATFPNGTRGVTLWRIAQEN-----HAAQQVLT 163

QY 164 V-----NCTAMASKPATITRMKGNTEKLSKSEVSEMSDMYVTSQMLMKVAKEDD 214
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

DB 164 IEPQSVAVARCVSTGRRPARITWISSLGEAKTOQEPIQAGVTITISRYLVVERAD 223

```
QY 215 GYFVLCQVHEHPAVTGNLTQRYLEVQYKPOVHIQMTYPLQGLTRGDALLETCEAIKRPQ 274
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 224 GYKVCRCVHEHSFEERILLPVTLSVRYPEVVIS-GYDDNMYLGRSEAI-LTCDVRSNPE 281

QY 275 PVMVTVAVRDEMPQAHVLSGNPLFINNLKNDNGTCRCASNIYGAHSDYMLVYDPT 334
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 282 PFDYMTSTTSGVFPASAAQGSQLVHSDVKRNVNTFTCTINNAVGTGAAQVILYRES 341

QY 335 TTTPPTTTTTTTTTTTTTTTTTTTTTIITDSRAGEEGSIRAVDHAIVGVAVV 385
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 342 ST-----AGAGATGTG-----IGGIHAII 361
```

RESULT 6

A44194
poliovirus receptor (clone AGM-alpha-1) - green monkey
C/Species: Cercopithecus aethiops (green monkey, grivet)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: A44194
R/Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotch, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A/Title: A second gene for the African green monkey poliovirus receptor that has no put.
A/Reference number: A44194; MUID:93059651; PMID:1331508
A/Accession: A44194
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-417 <KOI>
A/Cross-references: GB:S48777
C/Superfamily: poliovirus receptor; immunoglobulin homology
C/Keywords: transmembrane protein
F,259-314/Domain: immunoglobulin homology <IMM>

Query Match 10.7%; Score 244; DB 2; Length 417;
Best Local Similarity 23.5%; Pred. No. 7.2e-10;
Matches 108; Conservative 70; Mismatches 192; Indels 90; Gaps 18;

```
QY 13 AAAAAAAPGRLRLLLLFSAALIPDGDQNLFTKDYTV--IEGEVATISC--QVNK 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2  ARTMAAMP-----LTLTLELSMPPGGDIIVQAPTVGPGLGDSVTLPCVLQVPG 55

QY 69 SDDSVIQLNPNR-----QTIYFRDPRPLKDSRFOLNPFSSSEIKVSLTNVS-----I 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 56 MEETHVSQLTWSRHGESSMAVFHQTOGPVNSSEPRLEFVAFRLGTLELDASLRMFLRV 115

QY 117 SDEGRYFCQYTPDQESVYT--ITVAVPPRNLMIDIQDITAVEGEIEV--NCTAMASK 172
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 116 EDEGNYTC-LVTFPQGSRSYDWMRLVAKQN-TAEVQK-VQLNGKVPARCVSTGGR 172

QY 173 PATTTRMKGNTEKSGKEVEE---WSDKTYTTSQMLMKVAKEDDGVVLCQVHEHPAVT 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 173 PRAHITW---HSDLGCMNTEQAPGLFSGTIVVLSMLIVSSQVDGKSVCKVHEHSFE 229

QY 229 GNLQTORYLEVQYKPOVHIQMTYPLQGLTRGDALLETCEAIKRPQVMTVAVRDEMP 288
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 230 KQOLITVLTIVYPREVIS-GYDDNMYLSQNEA-TLTCDARSNDPFGYMTSTMGLP 287

QY 288 GHAVLSGNPLFINNLKNDNGTCRCASNIYGAHSDYMLVYDPTTTPPTTTTTTTTT 348
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 288 PRAVAQGAQLLRIPDKRINTTFICNVTNALGAQAEVTVQKSGPSPSGMSN----- 343

QY 349 TTTTILTIITDSRAGEEGSIRAVDHAIVGVAVVAVFAMLCILITL-----GRYFAHK 403
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 344 -----TITLLIGIVLLTLLIGIVFYRSR 369

QY 404 GT-----YFTHAKGADDAADDTIINABGGQNNSEKKE 439
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 370 CSREFLMCHILSPSSEEHASA-----SANGYISYSDVGRE 404
```

RESULT 7

HLMSF3

poliovirus receptor homolog precursor - mouse
 C/Species: Mus musculus domesticus (western European house mouse)
 C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
 C/Accession: A38211
 R/Morrison, M.E.; Racanelli, V.R.
 J. Virol. 66, 2807-2813, 1992
 A/Title: Molecular cloning and expression of a murine homolog of the human poliovirus re
 A/Reference number: A38211, MUID:92219365, PMID:1560525
 A/Accession: A38211
 A/Molecule type: DNA
 A/Residues: 1-467 <MOR>
 A/Cross-references: GB:M80206; NID:g19785; PIDN:AAA9734.1; PID:g199786
 C/Superfamily: poliovirus receptor; immunoglobulin homology
 C/Keywords: duplication; glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-467/Product: poliovirus receptor homolog #status predicted <MAT>
 F:26-334/Domain: extracellular #status predicted <EXT>
 F:47-133/Domain: immunoglobulin homology <IMM1>
 F:167-231/Domain: immunoglobulin homology <IMM2>
 F:267-322/Domain: immunoglobulin homology <IMM3>
 F:355-374/Domain: transmembrane #status predicted <TMN>
 F:375-467/Domain: intracellular #status predicted <INT>
 F:54-113,174-229,274-320/Dsulfide bonds: #status predicted
 F:128,138,315/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 10.7%; Score 244; DB 1; Length 467;
 Best Local Similarity 21.0%; Pred. No. 8.3e-10;
 Matches 101; Conservative 74; Mismatches 201; Indels 104; Gaps 16;

QY 15 AAAAAAPG-----LRLRLLLLSAALIPFGDGNLFTKQVTEGEV---ATISQV 66
 DB 2 ARAAVLPFSLSLPTLPPLLL-----LLETGADVAVRVLPEVRGLGVTBPCPL 56
 QY 67 -----NKSDDSVIQLINPNRQTIYFRDPRPKDSRFQI-----INFSS 105
 DB 57 LPEPTERVSGVTVQRDLGTVAAPFHS-----FGVDPSNQSFGKRLSFVARPEINADLR 112
 QY 106 ELKVSILTVSISDEGRYFQQLYTD--PQESYTTIVLVPPRLMIDIOKDAVEGEIE 163
 DB 113 DAIPLAFRGLRVEDEGNTCEFAFPNGTRGRVTLVLAQPE-----HARAEVT 163
 QY 164 V-----NCTMAKSPATTIRWPKG-NTELKGESEWSDMYVTLSQMLKYHKEDD 214
 DB 164 IGGQSAVAVACVSTGGRPARITWISLSGEAKDTQEPGIQAGTVITIIIRYSLVPGRAD 223
 QY 215 GVPVTCQVHPAVTGNLQTORLYEVQKQVHIQMTYPLQGLTRBGDALEITCEAIKFGQ 274
 DB 224 GVKVTCQVHESEFEPEILLPVLTSVRYPPPEVIS--GYDNWYLGREDAI-LTCDVRSNPE 281
 QY 275 PVAWTVWRVDEMPQHAVALSGPMLFINLNKKTNGYRCASNVIGKASDMLVYVDDP 334
 DB 282 PTBYDMSITSGVFPASNAVQSGQLVHSDRAMNTFTCTATNAVGTGAEGVILVYDIF 341
 QY 335 TTTPPTTTTTTTTTTTTTTTTTITDSRAGEGSGIRAVDHAIVGVAVVVA--MLCL 392
 DB 342 QA-----SR-----DVGPLVWAGVGGTLVLLLAGGLAI 372
 QY 393 IILGRYARHKGYTFHEAKGADA-----ADAPTAIINAGGQNNSEKXE 439
 DB 373 LILGRRRRRKSPGGGQDGDGRGYDPTQVFGNGGPFVFRSASBPFRPGRGDEDEEBE 432

RESULT 8
 JE0099
 neutral cell adhesion molecule 1 - African clawed frog
 N/Alternate names: N-CAM 1
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
 C/Accession: JE0099
 R/Xudo, M.; Takakuma, T.; Shiohawa, K.
 Biochem. Biophys. Res. Commun. 245, 127-132, 1998
 A/Title: Molecular cloning of ssd-form neutral cell adhesion molecules (N-Cams) as the ma
 A/Reference number: JE0099; MUID:96204770; PMID:9535795

A/Accession: JE0099
 A/Molecule type: mRNA
 A/Residues: 1-725 <KXD>
 A/Cross-references: DDBJ:AB008162; NID:g3116226; PIDN:BA25531.1; PID:g3116227
 A/Experimental source: heart
 C/Comment: This protein mediates and regulates various cell-cell interactions through bo
 C/Superfamily: neutral cell adhesion molecule; fibronectin type III repeat homology; immu
 F:413-475/Domain: immunoglobulin homology <IMM>
 F:512-589/Domain: fibronectin type III repeat homology <3FR>

Query Match 10.6%; Score 243; DB 2; Length 725;
 Best Local Similarity 26.5%; Pred. No. 1.7e-09;
 Matches 90; Conservative 61; Mismatches 147; Indels 42; Gaps 15;

QY 50 KDVTIVGEVATISCC---QVN---KSDSVIQLIN-----FNROTIFRDPKDSRFQI 99
 DB 199 KDQIVTVWPTTIGARLRNATAKMAESVYLSGADGFPDPIISMLKKEPIEDEE-EK 257
 QY 100 LNFSSSLKVSILTVSISDEGRYFQQLYTDPPQESYTTIVLVPPRLMIDIOKDAVAG 159
 DB 258 ISFNEDESEMTIHVEKDDAEVSC-IANNQAEAEATILKVAARKTIYENKTAVEL 316
 QY 160 EEIENVCTAMAKSPATTIRW-----FKNTELGKSEVEWSDMYVTLSQMLKYHKE 212
 DB 317 DEITLTCEA-SGDPISITRTAVRNISSEATLIDGHIYKHIIR-----SALTLDIOY 371
 QY 213 DDGVVTCQVHPAVTGNLQTORLYEVQKQVHIQMTYPLQGLTRBGDALEITCEAIK 272
 DB 372 TDAGEYFCIASNP-IGVDMQAM-YFEVQYAPKIR-----GVVVYTWEGNPNVITCEVFAH 425
 QY 273 PQPMVTWVAVDDMPQH-----AVLSGP---MLFINLNKKTNGYRCASNVIGKAS 324
 DB 426 PR-AAVTWFDGQLPESNSNITKIYSGPSSSLEVPDSENDFGNINCTAINTIHERS 484
 QY 325 DYMLVYVDPPTIIPPTTTTTTTTTTTTTTTTTITDSRAG 364
 DB 485 EFLVQADTPSS--PAIRKVEPYSSVWMLVPDEPSTGG 521

RESULT 9
 168093
 PRR2 delta - human
 C/Species: Homo sapiens (man)
 C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
 C/Accession: 168093
 R/Berle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
 Gene 159, 267-272, 1995
 A/Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is ch
 A/Reference number: 153960; MUID:95347610; PMID:7622062
 A/Accession: 168093
 A/Status: Preliminary; translated from GB/EWBL/DBd
 A/Molecule type: mRNA
 A/Residues: 1-538 <RES>
 A/Cross-references: GB:S79172; NID:g1042204; PID:g1042205
 C/Genetics:
 C/Superfamily: poliovirus receptor; immunoglobulin homology
 F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 10.6%; Score 242.5; DB 2; Length 538;
 Best Local Similarity 22.6%; Pred. No. 1.3e-09;
 Matches 111; Conservative 66; Mismatches 202; Indels 113; Gaps 17;

QY 10 SOCAAAAAAPRLRLLLLSAALIPFGDGNLFTKQVTEGEVATISQVNS 69
 DB 2 ARAAALPSPSPPLMLPILLL-----LLETG-ADQVRYQVLPVRG-----QLGCT 49
 QY 70 DDSVITQLNP-----NQTIYFRDPRPKDSRF-----QLNFS 104
 DB 50 VELPCHLLPVPGLYISLVWQRPDAPAHQNV--AAFHKMPSPSPSGSERISFVS 107
 QY 105 S-----ELKVSILTVSISDEGRYFQQLYTD--PQESYTTIVLVPPRLIMI 149

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Db      108 AKOSTGQDTEAEIQLDATALHGLTVDESNNTCEFAFPKGSVGNMTLRIATAKPRN-QA 166
      150 DIQKDTAVEGEIEIENVTAMASKPATITIRMPKG-NTELKSGSEVEEMSDMTYTSQMLMK 208
      167 EAKQTFESQPTTVALCISKEGRRPARISMLSLDEAKETQVSGTLACTVTVTSRFTLV 226
      209 VHKEDGVPVTCQVEHPAVTGNLQIQRYLEVQYKPOVHIQMTYPLQGLTRBGDALELTCE 268
      227 PSGRAGGVTVTCVKEHSESEEPALIPVTLISVRYPEVVIS-GYDDNMYLGRITDA-TLSCD 284
      269 AICKPOVAVMTWVRVDEMPQHAVLSGPNLFINNLKNTNGTGRCSASNIIVGAHSDYML 328
      285 VRNPEPTGDNSTGTFSTSAVAGSQVLIAVDSLNTTIVCTVITNAVGMGRAEQVI 344
      329 VYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTTTSDRAGEEGSIRAVDAVIGVAVVVFPM 388
      345 FVAREPTNT-----AGAGATGGI-----IGGIIMAILIATA 373
      389 LCILLILGRFAHKGITFHEAKGADDAAD-----TATINE-----G 429
      374 VAATGILICQOQKEQT-----LQGAEBEDLEGGPSYKPPTKALEQEMPSQLFTLG 428
      430 GQNNSEKKEVF 441
      429 ASHSPSLKTPYF 440

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RESULT 10

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B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C:Species: Cercopithecus aethiops (green monkey, grivet)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: B44194
C:Virol. 66, 7059-7066, 1992
R:Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotch, O.; Nomoto, A.
A:Title: A second gene for the African green monkey poliovirus receptor that has no putative
A:Reference number: A44194; MUID:93059651; PMID:1331508
A:Accession: B44194
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-392 <KOI>
A:Cross-references: GB:S48817
F:Superfamily: poliovirus receptor; immunoglobulin homology
F:259-314/Domain: immunoglobulin homology <IMM>

```

```

Query Match      10.6%; Score 241.5; DB 2; Length 392;
Best Local Similarity 24.0%; Pred. No. 1e-09;
Matches 101; Conservative 60; Mismatches 178; Indels 81; Gaps 16;

```

```

      13 AAAAAAAPGRLRLRLLLLFSAALIPGQGNLFTKDVTV--IEGEVATISC-QVNK 68
      2  ARTMAAAMP-----LLLTLELSWPPPGTGDIIVQAPQVPGFLDSTVTLPCYQVPG 55
      69 SDDSVIQLNPNR-----QTIYRDFRPLKDSRFQNLNFSSELKXSLTVNS-----I 116
      56 MEETHVQLTWRSRSGESMAVPHQIQGPNYSEPKRLEFVAARLGTGLRNASLRMGRLV 115
      117 SDEGRYFCQIYTDPPQESYTT---ITVLVPPRNLMDIQKDTAVEGEIEV-NCTAMASK 172
      116 EDEBNYTC-LFVTFPQGSRSVDIWLRLAPQN-TAEVQK-VQLTGFPVAVACVSGGR 112
      173 PATTIRFKGNTLKGSEVEE---MSDKTTSQMLKXHKEDDGVPIYCOVEHPAVT 228
      173 PPAHITW---HSDIGGMPNTSQAPGFLSGVTVTSLMILVPSQVDSKSTVCKVEHSFE 229
      229 GNLQTRLEYQYRQVHIQMTYPLQGLTRBGDALELTCEAIKQPOVAVMTWVRVDEMP 288
      230 KPQLITVNLTVIYYPEVIS-GYDNNWYLGQNEA-TITCDARSNPEFTGNNMTMGLP 287
      289 QHAVLSGNLFINNLKNTDNGTYRCEASNIIVGAHSDYMLVYVDPPTTTPPTTTTTTT 348
      288 PFAVAGQQLIRPVDKPIINTTFICNVTNALGARQAEITVQVKEGPESEBSGMSNN--- 343

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      349 TTTTTLITITDSRAGEEGSIRAVDAVIGVAVVVFAMLCILLI-----GRYFAHK 403
      344 -----IIIFILGIVLITLLIGIVFYRSR 369

```

RESULT 11

```

poliovirus receptor splice form delta precursor - human
N:Alternate names: poliovirus receptor H20B
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997
C:Accession: A43024; B31496
R:Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Takeuchi, Y.
A:Title: The poliovirus receptor protein is produced both as membrane-bound and secreted
A:Reference number: S12048; MUID:51006015; PMID:2170108
A:Accession: A43024
A:Molecule type: DNA

```

```

A:Residues: 1-392 <KOI>
A:Cross-references: EMBL:X64116
A:Note: 67-Ala was also found
R:Wendelsch, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A:Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and
A:Reference number: A90910; MUID:89168426; PMID:2538245
A:Accession: B31496
A:Molecule type: mRNA
A:Residues: 1-66, 'A', 68-392 <MEN>
A:Cross-references: GB:W24406
A:Comment: The normal function of this receptor is unknown. Membrane-bound and soluble
C:Genetics:
A:Gene: GDB:PVR; PVS
A:Cross-references: GDB:120324; OMIM:173850
A:Map position: 19q13.2-19q13.2
A:Antons: 27/1, 143/1, 242/1, 281/2, 331/1
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pr
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-392/Product: poliovirus receptor delta #status predicted <EXT>
F:21-143/Domain: extracellular #status predicted <EXT>
F:42-125/Domain: immunoglobulin homology <IMM1>
F:159-223/Domain: immunoglobulin homology <IMM2>
F:259-314/Domain: immunoglobulin homology <IMM3>
F:344-367/Domain: transmembrane #status predicted <TMN>
F:368-392/Domain: intracellular #status predicted <INT>
F:49-123, 166-221, 266-312/Disulfide bonds: #status predicted
F:105, 120, 188, 218, 237, 278, 307, 313/Binding site: carbohydrate (Asn) (covalent) #status p

```

```

Query Match      10.5%; Score 240; DB 1; Length 392;
Best Local Similarity 25.9%; Pred. No. 1.3e-09;
Matches 107; Conservative 54; Mismatches 176; Indels 76; Gaps 17;

```

```

      14 AAAAAAAPGRLRLRLLLLFSAALIPGQGNLFTKDVTV--IEGEVATISC- 64
      2  ARMAAAMPVLLIALLVLSWP-----PQGTG-----DVVQAPQVPGFLDSTVTLPCY 50
      65 -QVNSDSDSVIQLNPNR-----QTIYRDFRPLKDSRFQNLNFSSELKXSLTVNS-- 115
      51 LQVPMNEVTHVQLTWTRHSGESMAVPHQIQGPNYSEPKRLEFVAARLGTGLRNASLRM 110
      116 -----ISDEGRYFCQIYTDPPQESYTT---ITVLVPPRNLMDIQKDTAVEGEIEV-NCT 167
      111 FGLRVDEBNYTC-LFVTFPQGSRSVDIWLRLAPQN-TAEVQK-VQLTGFPVAVACVSGGR 167
      168 AMASKPATITIRFKGNTLKGSEVEE-SDMYTTSQMLKXHKEDDGVPIYCOVEHPA 226
      168 STGSRPPAQTWASHLGGMPNTSQVPGFLSGVTVTSLMILVPSQVDSKSTVCKVEHS 227
      227 VTGNLQTRLEYQYRQVHIQMTYPLQGLTRBGDALELTCEAIKQPOVAVMTWVRVDE 286
      228 FKPQLITVNLTVIYYPEVIS-GYDNNWYLGQNEA-TITCDARSNPEFTGNNMTMGLP 285
      287 MQHAVLSGNLFINNLKNTDNGTYRCEASNIIVGAHSDYMLVYVDPPTTTPPTTTTTT 346

```


Db 372 TDAGEYFCIASNF-IGVDQAM-YFEVQYAPKIR-----GPVVVYTWEGNPVNITCEVFAH 425

QY 273 PQVWVWTVWRVDEMPQH-----AVLSGP---NLFINNLTNDNGYRCEASNIYKXHS 324

Db 426 PR-AAATWYFSDGQLPSSNFSNFKIYSGFTSSSEVENPDSNDFGNVCTAINTTGHFS 484

QY 325 DYMLVYVDPPTTIPPTTT 364

Db 485 EPIVQADTPSS---PAIRKVEPYSSTWIVFDEPSTG 521

RESULT 14

connectin/ctitin - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C/Accession: T42633
R: Tajima, H.; Onosuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.; Ma
Biochem. Biophys. Res. Commun. 223, 160-164, 1996
A/Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/ctitin re
A/Reference number: Z22221, MUID:96254045, PMID:8660363
A/Accession: T42633
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-4162 <YAJ>
A/Cross-references: EMBL:D83390; NID:G1513029; PIDN:BA11908.1; PID:G1513030
A/Experimental source: breast muscle
C/Keywords: skeletal muscle

Query Match 10.1%; Score 230.5; DB 2; Length 4162;

Best Local Similarity 23.9%; Pred. No. 1.3e-07; Indels 59; Gaps 15;

Matches 86; Conservative 60; Mismatches 155;

Db 12 CAAAAAARPPGLRLRLLLLSAALIPTGQDQNTFTQDVYIEGEVATISQVKSDD 71

Db 3453 CIGSVTLRAPFTFVKUL-----SDVTYVVGETIELQAAVEGAQP 3491

QY 72 SVIQLNPNRQTIYFRPRLKDSRQQLNFSSELKSLTNVISDEGRYFQQLYTDPP 131

Db 3492 ISVWLKDKGEIT-----RESENLWISYSENVASLKTGNAPFTNAGRYICQIKNDAG 3543

QY 132 -QESYTTITVLVPPRNIMIDIOKDTAVE---GEEIEVNCTAMASKPATIIRWEKNTLEK 187

Db 3544 FQCFKALTYLDP---AVIVEKPGPVKTAGDSCTLECT-VDTPELTARWFKDGNELS 3598

QY 188 GKSEVEWSDMYVTSQMLKVKHKEDG--VPYICQVEHPAVTGNLQ-TQRYLEVQYKP 243

Db 3599 TDHXY-KISFFNKVSGLKIINAGLEDSEYTFEKNVSGKSCIASLOVSDRIMPPSFT 3657

QY 244 QVHQMYYPLQGLTBEGDALELTCEALGKPOVMTWVRVDDMPQ---HAVLSGP--N 297

Db 3658 K--LKETY-----GQLSSAVLECKYVGP-PIIVSWFHGQBITSGDKYQALTLTNTCS 3709

QY 298 LFINNLTNDNGYRCEASNIYKXHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTT 355

Db 3710 LKVMGLQESDMGYSCATNVAGSDCEASFLSVREPPSFVKKPEFNVLSGENITFTSIV 3769

RESULT 15

156551

neurotrophin - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C/Accession: 156551

R: Struyk, A.F.; Canoll, P.D.; Wolgast, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J.L.

J. Neurosci. 15, 2141-2156, 1995

A/Title: Cloning of neurotrophin defines a new subfamily of differentially expressed neur

A/Reference number: 156551, MUID:95198094, PMID:7851157

A/Accession: 156551

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-344 <RES>

A/Cross-references: EMBL:U16845; NID:G755184; PIDN:AAA67445.1; PID:G755185

C/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 10.1%; Score 230; DB 2; Length 344;

Best Local Similarity 26.2%; Pred. No. 5.6e-09; Indels 46; Gaps 14;

Matches 84; Conservative 53; Mismatches 137;

Db 29 LLLLSAALIPTGQDQNLFTK--DYVIEGEVATISQVKSDDSVIQLNPNRQTI- 84

Db 19 LRLFLVPTGVVPSGDATEPKAMDVTYRQGESATLRCTI---DNRVTEVAMLRSTIL 75

QY 85 YFRDPRPLKDSRQQLNFSSELKSLTNVISDEGRYFQQLYTD-PPQSYTTITVLVP 143

Db 76 YAGNDKWCIDPRVVLNSTCTQISIEIQNDVDYDEGPTYSVQIDNFKISRHLIYQS 135

QY 144 PRNIMIDIOKDTAV-EGEEIEVNCTAMASKPATIIRFKNTLEKSGSEVEWSDMYT 202

Db 136 PK--IVEISSDISINEGNISLTCLIA-TGRPEPTVTRHISPKAVGVSEDEYLEIQIT 192

QY 203 SOLMLKVAH--KEDDGVPIQVHPAVTGNLQTCRYLEVQYKQVHICMTYPLQGL-TR 258

Db 193 REQGEYECASNDVAAVVRVN-----VTNVPPYIS-----EAKGTGVP 234

QY 259 EGDALLETCEALGKPOVMTWVRVDDMPQ-----HAVLSGPNLFINNLTNDNG 309

Db 235 VGQKGTLOCESAVPS-AEPQMFKDDKRLVGGKGVKVENRPFSLRLTF--NVSEHDYG 291

QY 310 TYRCEASNIYKXHSDYMLY 329

Db 292 NYTCVASNKLGHNTASIMLF 311

Search completed: July 7, 2004, 06:00:27

UDB time : 34.7249 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 ; Search time 29.126 Seconds
(without alignments)
790.187 Million cell updates/sec

Title: US-10-622-237-2
Perfect score: 2283
Sequence: 1 MASVILPSSGSCCAAAAAA.....AIIINAQGQNNSEKEYFI 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	266.5	11.7	515	1 PVR1_PIG	Q9G176 sus scrofa
2	256.5	11.2	517	1 PVR1_HUMAN	Q15223 mus musculus
3	247.5	10.8	530	1 PVR2_MOUSE	P32807 mus musculus
4	244	10.7	417	1 PVR2_MOUSE	P32806 cercoptidic
5	242.5	10.6	538	1 PVR2_HUMAN	Q92892 homo sapien
6	240	10.5	417	1 PVR1_HUMAN	P15151 homo sapien
7	239	10.5	515	1 PVR1_MOUSE	Q9J4F6 mus musculus
8	239	10.5	1088	1 NCAL_XENLA	P16170 xenopus lae
9	231	10.1	344	1 NTR1_MOUSE	Q99510 mus musculus
10	230	10.1	344	1 NTR1_HUMAN	Q62718 ratius norv
11	228	10.0	344	1 NTR1_MOUSE	Q9P121 homo sapien
12	223.5	9.8	837	1 NCW2_MOUSE	O35136 mus musculus
13	223	9.8	1092	1 NCAL_XENLA	P36335 xenopus lae
14	222	9.7	837	1 NCW2_HUMAN	O15394 homo sapien
15	222	9.7	1242	1 NPHN_MOUSE	Q9G267 mus musculus
16	219	9.6	337	1 OPCW_CHICK	Q98892 gallus gall
17	218.5	9.6	343	1 OPCW_BOVIN	P11834 bos taurus
18	217.5	9.5	583	1 C166_MOUSE	Q61490 mus musculus
19	217	9.5	588	1 C166_CHICK	P42292 gallus gall
20	216.5	9.5	345	1 OPCW_HUMAN	Q14982 homo sapien
21	213.5	9.4	4391	1 PGBW_HUMAN	P98160 homo sapien
22	210.5	9.2	345	1 OPCW_RAT	P32736 ratius norv
23	209	9.2	338	1 LAMP_CHICK	Q98919 gallus gall
24	209	9.2	353	1 CEPY_CHICK	Q90773 gallus gall
25	208	9.1	1493	1 NEOL_MOUSE	P97798 mus musculus
26	207	9.1	847	1 CD22_HUMAN	P20273 homo sapien
27	206.5	9.0	1331	1 CTA2_HUMAN	Q9UNC6 homo sapien
28	206	9.0	702	1 CEAS_HUMAN	P06731 homo sapien
29	205.5	9.0	338	1 LAMP_HUMAN	Q13449 homo sapien
30	205.5	9.0	509	1 SHS1_RAT	P97710 r protein-t
31	205.5	9.0	646	1 MUI8_HUMAN	P43121 homo sapien
32	205.5	9.0	1461	1 NEOL_HUMAN	Q92859 homo sapien
33	204	8.9	3707	1 PGBW_MOUSE	Q05793 mus musculus

34	202.5	8.9	862	1 CD22_MOUSE	P35329 mus musculus
35	202	8.8	1377	1 NEOL_RAT	P97603 ratius norv
36	202	8.8	1443	1 NEOL_CHICK	Q90610 gallus gall
37	199.5	8.7	338	1 LAMP_RAT	Q62813 ratius norv
38	199.5	8.7	1241	1 NPHN_HUMAN	Q60500 homo sapien
39	197.5	8.6	1234	1 NPHN_RAT	Q97044 ratius norv
40	197	8.6	583	1 C166_HUMAN	Q13740 homo sapien
41	196	8.6	1091	1 NCAL_CHICK	P13590 gallus gall
42	194	8.5	506	1 SHS1_BOVIN	Q46631 bos taurus
43	193	8.5	761	1 NCAL2_HUMAN	P13582 homo sapien
44	193	8.5	764	1 ICCR_DROME	Q08180 drosophila
45	193	8.5	848	1 NCAL_HUMAN	P13591 homo sapien

ALIGNMENTS

RESULT 1	ID	PVR1_PIG	STANDARD	PRT	515 AA
AC	Q9G176				
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Poliiovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (Hvrc) (Nectin 1).				
DE	PVR1 OR PVR1 OR HVRC.				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_TaxID=9623;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=21176378; PubMed=11277703;				
RA	Miller R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,				
RA	Cohen G.H.,				
RT	"Porcine Hvrc, a member of the highly conserved Hvrc/nectin 1 family,				
RT	is a functional alphaherpesvirus receptor."				
RL	Virology 281:315-328(2001).				
CC	- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.				
CC	- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).				
CC	- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.				
CC	- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.				
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CC	EMBL: AF308632; AAC30281.1; -				
DR	HSSP: P06907; INEU				
DR	InterPro: IPR007110; Ig-like.				
DR	InterPro: IPR003596; Ig_v.				
DR	Pfam: PF00047; Ig_2.				
DR	SMART: SMO0406; IGV; 1.				
DR	ProSITE: PS50835; IG_LIKE; 2.				
KW	Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane; Repeat; Glycoprotein; Signal.				
FT	SIGNAL	1	30		POTENTIAL.
FT	CHAIN	31	515		POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
FT	CHAIN	31	515		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	356	376		POTENTIAL.
FT	DOMAIN	377	515		CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	31	141		IG-LIKE V-TYPE.
FT	DOMAIN	145	243		IG-LIKE C2-TYPE 1.
FT	DOMAIN	247	334		IG-LIKE C2-TYPE 2.
FT	DOMAIN	437	443		POLY-GLU.

FT DOMAIN 444 447 POLY-GLY
 FT DISULFID 51 124 BY SIMILARITY.
 FT DISULFID 172 226 BY SIMILARITY.
 FT DISULFID 269 316 BY SIMILARITY.
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 515 AA; 57047 MW; BFA00320DEDC3785 CRC64;

Query Match 11.7%; Score 266.5; DB 1; Length 515;
 Best Local Similarity 24.8%; Pred. No. 9e-12;
 Matches 108; Conservative 63; Mismatches 163; Indels 101; Gaps 18;

QY 52 VTVEBEVATISQVAKSDSVTLQNLNPNROTIFRFRPLKDSRFOLINPSSSELYSL 111
 DB 62 ITQVTQKATNGSKQK-----VAIYNPAMGVSVLAPYR-----ERVEFLRPFDTGTIRL 111
 QY 112 TNVISDEGRYPCQLYTDP--QESYTTTVALPPNIMIDQ-----KDTAVEGE 161
 DB 112 SRLEDEGVYICEFATPPAGNRESQJLNTMAKPTNIEGTQAVLRAGKGDYV--- 167
 QY 162 IEVNTAMASKPATITRFKGNTELKSEVEEM--SDMTVTSQMLKVKHEDGYPV 218
 DB 168 LVATCTISANGKPSVSW---ETHLKGEAEYOEINPNCTVVISRYRLVPEREDHQS 224
 QY 219 TCVHEPANTGNLTQRY---LEVQYKPOVHIQ---MTYLGQLTREGDALETCAT 270
 DB 225 ACTV-----NYHMDRFRESITLNLQVPEVTIEBFQDNWYLOMD-----VKLTQCAD 272
 QY 271 GKQPMVMTVVRVDDEPOHVAVSGNLFINN-LNKTDGTRCEASNTVGKASHDYMLY 329
 DB 273 ANPAPHEHMTTNGSLPKGVENQNTLFFRGPINVSAGTICENTNIPIGRSQVENV 332
 QY 330 VVDEPTTPTPTTTTTTTTTTTTTTTTTTTTTITDSPACEGSGIRAVNAVIGVVA--VVVF 386
 DB 333 ITFPTPTSPPE-----HGRRAQ-----VPTAIGGVGSILVLF 369
 QY 387 AMCLIIIGRYFARHKTGYFT-----HEAKG-----DPAADADYAI 424
 DB 370 VVGGIIVALLCRHHTKDYSTKHYNGYSGACIPQHHPMAQNLQYPEDSDDEKA- 428
 QY 425 INAEGQNNSEKKE 439
 DB 429 -GPGSSYEHEEE 442

RESULT 2
 PVRL_HUMAN STANDARD; PRT; 517 AA.
 ID PVRL_HUMAN
 AC Q15223; Q75465; Q9HBE6; Q9HBM2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
 mediator C) (HvEC) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)
 DE (CD11 antigen).
 GN PVRL OR PRL OR HVEC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_Taxid=9606;
 RN 11)
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=95237621; PubMed=7721102;
 RA Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
 RA Dubreuil P.;
 RT "CDNA characterization and chromosomal localization of a gene related
 RT to the poliovirus receptor gene.";

RL Gene 155:261-265 (1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=98279152; PubMed=9616127;
 RA Geraghty R.J., Krumenacher C., Cohen G.H., Eisenberg R.J.,
 RA Spear P.G.;
 RT "Entry of alphaherpesviruses mediated by poliovirus receptor-related
 RT protein 1 and poliovirus receptor."
 RL Science 280:1618-1620 (1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
 RX MEDLINE=21256041; PubMed=11356977;
 RA Lopez M., Cocchi F., Avitabile B., Leclerc A., Adelaide J.,
 RA Campadelli-Fiume G., Dubreuil P.;
 RT "Novel, soluble isoform of the herpes simplex virus (HSV) receptor
 RT nectin (or pr1-HvEC-HvEC) modulates positively and negatively
 RT susceptibility to HSV infection."
 RL J. Virol. 75:5684-5691 (2001).
 RN [4]
 RP SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
 RX MEDLINE=20392396; PubMed=10932188;
 RA Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
 RA Helms J.A., Spritz R.A.;
 RT "Mutations of PVRL1, encoding a cell-cell adhesion
 RT molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
 RT dysplasia."
 RL Nat. Genet. 25:427-430 (2000).
 CC -1- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
 CC ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
 CC CELLS.
 CC -1- SUBUNIT: Interacts with HSV glycoprotein D (gD).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
 CC delta). Secreted (isoform gamma).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=Delta;
 CC IsoId=Q15223-1; Sequence=Displayed;
 CC Name=Alpha;
 CC IsoId=Q15223-2; Sequence=VSP_002626; VSP_002627;
 CC Name=Gamma;
 CC IsoId=Q15223-3; Sequence=VSP_002624; VSP_002625;
 CC -1- DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-
 CC ectodermal dysplasia syndrome (CLPEDI) [MIM:225000]. CLPEDI is
 CC responsible for allelic forms known as Margarita island ectodermal
 CC dysplasia [MIM:225060] and Zlotogora-Oguz syndrome.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -1- DATABASE: NAME=PROV; NOTE=PROV 2:45-49 (2001);
 CC WWW=http://www.ncbi.nlm.nih.gov/prov/guide/2005693930.g.htm".
 CC -----
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 CC -----
 DR EMBL, X76400; CA53980.2; ALT_INIT.
 DR EMBL, AF060231; AAC23798.1; -.
 DR EMBL, AY029539; AA03124.1; -.
 DR EMBL, AF252867; AA016648.1; -.
 DR EMBL, AF196768; AA016648.1; JOINED.
 DR EMBL, AF196769; AA016648.1; JOINED.
 DR EMBL, AF196770; AA016648.1; JOINED.
 DR EMBL, AF196771; AA016648.1; JOINED.
 DR EMBL, AF196774; AA016649.1; -.
 DR EMBL, AF196768; AA016649.1; JOINED.
 DR EMBL, AF196769; AA016649.1; JOINED.
 DR EMBL, AF196770; AA016649.1; JOINED.
 DR EMBL, AF196771; AA016649.1; JOINED.
 DR EMBL, AF196772; AA016649.1; JOINED.
 DR EMBL, AF196773; AA016649.1; JOINED.


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DR Genew: HGNC:9706; PVRL1.
DR MIM: 600644; -.
DR MIM: 225000; -.
DR GO: GO:0016021; C: integral to membrane; NAS.
DR GO: GO:0004895; F: cell adhesion receptor activity; NAS.
DR GO: GO:0015026; F: coreceptor activity; TAS.
DR GO: GO:0006955; P: immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS00835; IG_Like; 2.
KM Cell adhesion: Immunoglobulin domain; Receptor; Transmembrane;
KM Repeat; Glycoprotein; Signal; Alternative splicing.
FT CHAIN 1 30
FT SIGNAL 1 30
FT CHAIN 31 517
FT DOMAIN 31 355
FT TRANSMEM 356 376
FT DOMAIN 377 517
FT DOMAIN 31 141
FT DOMAIN 149 238
FT DOMAIN 247 334
FT DOMAIN 437 444
FT DOMAIN 445 449
FT DISULFID 51 124
FT DISULFID 172 226
FT DISULFID 269 316
FT CARBOHYD 36 36
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 202 202
FT CARBOHYD 286 286
FT CARBOHYD 297 297
FT CARBOHYD 307 307
FT CARBOHYD 332 332
FT CARBOHYD 335 352
FT VARSPLIC 353 517
FT FTID=VSP 002624.
FT Missing (in isoform Gamma).
FT VARSPLIC 336 458
FT FTID=VSP 002625.
FT Missing (in isoform Gamma).
FT VARSPLIC 459 517
FT FTID=VSP 002627.
FT Missing (in isoform Alpha).
SQ SEQUENCE 517 AA; 57158 MW; DF34CBAEC893EBED CRC64;
Query Match 11.2%; Score 256.5; DB 1; Length 517;
Best Local Similarity 25.5%; Pred. No. 4.7e-11;
Matches 105; Conservative 60; Mismatches 154; Indels 93; Gaps 19;
QY 74 TQLNPNKQTYFPDPRFKLSDKSPQLNFSSEKSLTNVSIIDDERGYCQLYTPD-- 131
DB 78 VAIYPMKGVSVLAPYR---ERVEFLRPFSTDTIRLSRLLEDEGVYICEFYFPTGN 133
QY 132 QESTYTIIVLPRLMLDIOKD-TAVGEIEIV---NCTAMASKPATTTIRWFGNTELK 187
DB 134 RESQNLTVMAKPTWIGTQAVLRKKGGQDQKLVATCTISANKRPSVSM---ETRLK 190
QY 188 GKSEVEEN---SDMYTTSQMLKXHKEDGVYICVYEHFPAVTGNLQTORV-----LEV 235
DB 191 GEAEYOEIRNPNNGVTIVISRYRLVPSREAHQOOSLACIV-----NYHMDFKESLTLNV 243
QY 240 CYKPRVNHQ---MTYPLQGLRREGDALTECEATGKPKPVMWTVWVVDDEMKCHAVLSGP 296
DB 244 QIEPEVTIEGPDGNVYLDQRM-----VLTCKADANPAPTATYVHTTLNGSLPKVEAQR 298
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QY 297 NLFTLN-LNKTDNGTYRCEASNIYKKAHSDMYLVYDPTTPTTTTTTTTTTTL 355
DB 299 TLFFKGPINSLACTYICCATNPIGTRSGQVEVNTTFEPTSPHPE----- 344
QY 356 TIITDSRAGEBSIRANDHAVIGVAVVYFAMLCILIIIGRYA-----RH--KGYET- 408
DB 345 ---HGRAG-----PVPPLAIGVAGST---LVLIVGGIYVALRRRHTTFKGDYSTK 392
QY 409 -----HEAKGA-----DDAADTALINAGGONNSEKKE 439
DB 393 KHYVNGSKAGIPQHHPMAQNQYDDSDDEKKA--GPLGGSSYESEEE 442
RESULT 3
PVR2_MOUSE STANDARD; PRT; 530 AA.
ID PVR2_MOUSE
AC P32507.062096;
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Murine herpesvirus
DE entry protein B) (HvheB) (Nectin 2) (Poliovirus receptor homolog).
DE PVR2 OR PVS OR PVR OR MPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=92219365; PubMed=1560525;
RT Morrison M.E., Racanietello V.R.;
RT "Molecular cloning and expression of a murine homolog of the human
RT poliovirus receptor gene";
RL J. Virol. 66:2807-2813 (1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RX STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=94179228; PubMed=8132569;
RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
RT "Amino acid residues on human poliovirus receptor involved in
RT interaction with poliovirus";
RL J. Biol. Chem. 269:8431-8438 (1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RX STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., Morley K.C., McKernan K.D., Malek J.A., Gunaratne P.H.,
RA Richards S., Wooten R.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99214397; PubMed=10196354;
RA Shukla D., Rowe C.L., Dong Y., Racanietello V.R., Spear P.G.;
RT "The murine homolog (Mph) of human herpesvirus entry protein B (HvheB)
RT mediates entry of pseudorabies virus but not herpes simplex virus
RT types 1 and 2.";
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OY 106 ELKVSILNVSISSEGGYFQOLVTD--PQSEYTIITLVPPRNIMIDIQCDTAVEBEEI 163
DB 113 DAIARGLRVEDBEGYTCFEATFPNGRGVIMLRVIAQDEN-----HAEQSVT 163
OY 164 V-----NCTAMASKPATITRMFKG-NTELKKKSEVEWSDYVTVTQMLRVAKEDD 214
DB 164 IGFQSVAVARCVSTGGRFPARITWISSIGCEAKXDTQFQIAGTVIIISRYSLVPGRAD 223
OY 215 GAVPVIQVQHHPAVNTGNLQQRATLEQVQKQVQHICMTYPLQGLRREGDALELTGEAKGKQ 274
DB 224 GAVVTRVREHSEBEEPIILLPTLSVRYPEVIS-GYDDNMWYLRGSEAI-LTCDVRSNPE 281
OY 275 PWWVTWVRVDEMPQHAVALSGENFINNLTNDGTGRCAASNIVGKXSDYMLVYDDP 334
DB 282 PTDYDSTTSGVFAPASAVQSGQLVHSDVMWNTFTCTATNAGVGRAGQVILVRES 341
OY 335 TITPPTTTTTTTTTTITLITITDSAGEGSRVADHAVIGGVAVVY 385
DB 342 ST-----AGAGATGSI-----IGGIIMAIT 361

RESULT 4
PVR CERAE
ID PVR CERAE STANDARD: PRT: 417 AA.
AC P32506;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor.
PVR OR PVS.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).
RC TISSUE=Kidney;
RX MEDLINE=93059651; PubMed=1331508;
RA Koike S., Ise I., Sato Y., Yonekawa H., Gotoh O., Nomoto A.;
RT "A second gene for the African green monkey poliovirus receptor that
RT has no putative N-glycosylation site in the functional N-terminal
RT immunoglobulin-like domain."
RL J. Virol. 66:7059-7066(1992).
CC -1- FUNCTION: Not known. Used by poliovirus to bind and enter the
CC cell.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform alpha).
CC Secreted (isoforms beta and gamma).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P32506-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P32506-2; Sequence=Not described;
CC Name=Gamma;
CC IsoId=P32506-3; Sequence=Not described;
CC Name=Delta;
CC IsoId=P32506-4; Sequence=Not described;
CC IsoId=P32506-2; Sequence=VSP 002622, VSP 002623;
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC
CC EMBL; D12611; BA002136.1; -.
CC DB EMBL; D12612; BA002137.1; -.
CC PIR; A44194; A44194.

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DR PIR; B44194; B44194.
 DR InterPro: IPR007110; Ig-Like.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_3.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS00835; IG_LIKE; 3.
 KM Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; signal;
 KM Repeat; Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 417
 FT DOMAIN 21 343
 FT TRANSMEM 344 367
 FT DOMAIN 368 417
 FT DOMAIN 24 139
 FT DOMAIN 145 237
 FT DOMAIN 244 328
 FT DISULFID 49 123
 FT DISULFID 166 221
 FT DISULFID 266 312
 FT CARBOHYD 85 85
 FT CARBOHYD 120 120
 FT CARBOHYD 188 188
 FT CARBOHYD 237 237
 FT CARBOHYD 278 278
 FT CARBOHYD 307 307
 FT CARBOHYD 313 313
 FT VARSPPLIC 386 392
 FT VARSPPLIC 393 417
 SQ SEQUENCE 417 AA; 45464 MW; DA4AD0FE4D2F6B1F CRC64;
 Query Match 10.7%; Score 244; DB 1; Length 417;
 Best Local Similarity 23.5%; Pred. No. 2.8e-10;
 Matches 108; Conservative 70; Mismatches 192; Indels 90; Gaps 18;

13 AAAAAAPGRLRLILFLSAAALPTDQGLTKVTV--IGEVATISC--QNVK 68
 2 ARTPAAWMP-----LLTLLELSMPPETGDIIVQAPVQVGFAGDSVTLPCYLQVNG 55
 69 SDDSVIQLNPNR-----CTVFRDPRPLKDSRFQOLNFSSSLKVLTVNS-----I 116
 56 MEETHVQSGLTWSHGSGSMAVHQGPNVSEPKRIEFVAARLTGLRDAISLRFGLRV 115
 117 SDGGRVYCCQVYTPDPQSYTT---ITLVPRRLMDICQDTAVGEGEIEV--NCTAMAK 172
 116 EDEGNVYC-LFVTFPGGSRSDVIMRLVLRPN-TAEVQK-VQLTGKPVFARCVSTGR 172
 173 PATTFRFKNTLEIKGSEVE-----WSDMYVTLSQMLKVKHEDGVPIQCEHPAVT 228
 173 PPAHITM--HSDLGMPNLSQAPGLSGIVTVLSLIMLVPSQVQVGSKTVCVHESE 229
 229 GNIOTORYEVQKQVHIQNTYPLQGLTREGDLBELTCAIKGPOFVMTVTRVDEMP 288
 230 KPQLLTVALTVVYVPEVISI-GYDNMYLISQNEA-TLTCARSNPELTGVMSTWGFLP 287
 289 QHAYLGSFNLFINNLTNDNGYRCEASNTVKGASNYMUYVDDPTTPTTTT 348
 288 PRAVAQAQLIRVDPKPIITTFICVNTNALGARQALITVQVEGPPSSGSSN----- 343
 349 TTTTTLITTTDSFAGEGSIKAVDAVIGGVAVVFMCLILII-----GRYPAHK 403
 344 -----IIIFLLIGIVILLTLIGIVFYFRSR 369
 404 GT-----YETHAKGADDAADATIALINAGGQNNSEKKE 439
 370 CSRFLWCHHLSPSSEHSA-----SANGYISIVSRE 404

RESULT 5
 FVR2_HUMAN STANDARD; PRT; 538 AA.
 AC Q92692; C75455; Q96J29;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Poliovirus receptor related protein 2 precursor (Herpes virus entry
 DE mediator B) (HvEB) (Nectin 2) (CD112 antigen).
 GN PVR2 OR PRR2 OR HVES.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_Taxid=9606;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=95347610; PubMed=7622062;
 RA Eberle F., Dubreuil P., Mattei M.-G., Devillard E., Lopez M.;
 RT "The human PRR2 gene, related to the human poliovirus receptor gene
 (PVR), is the true homolog of the murine MPH gene."
 RL Gene 159:267-272(1995).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=96321161; PubMed=9657005;
 RA Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,
 RA Whitebeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;
 RT "A cell surface protein with herpesvirus entry activity (HvEB) confers
 RT susceptibility to infection by mutants of herpes simplex virus type
 RT 1, herpes simplex virus type 2, and pseudorabies virus."
 RL Virology 246:179-189(1998).
 [3]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsten F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brancosin M., Soares M.B., Bonaldi M.F., Casavant T.D., Scheetz T.E.,
 RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carrinetti P., Prange C.,
 RA Raba S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Boeck S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.W., Maitra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RP SEQUENCE OF 31-538 FROM N.A.
 RA Yoshitake K., Murray J.C.;
 RT "A transcriptional map in the region of 19q13 derived using direct
 RT sequencing and exon trapping."
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE OF 449-538 FROM N.A.
 RX MEDLINE=99449047; PubMed=10520737;
 RA Freitas E.M., Zhang W.J., Lalonde J.P., Tay G.K., Gaudieri S.,
 RA Ashworth L.K., Van Bockxmeer F.M., Dawkins R.L.;
 RT "Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene:
 RT PERC1."
 RL DNA Seq. 9:89-101(1998).
 CC - FUNCTION: RECEPTOR FOR ALPHABETAVIRUS (HSV-1, HSV-2 AND
 CC PSEUDORABIES VIRUS) ENTRY INTO CELLS.
 CC - SUBCELLULAR LOCATION: Type I membrane protein.
 CC - ALTERNATIVE PRODUCTS: Named isoforms=2;
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Delta;
 CC Name=Alpha;
 CC IsoId=Q92692-1; Sequence=Displayed;
 CC IsoId=Q92692-2; Sequence=VSP_002628, VSP_002629;
 CC

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CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- DATABASE: NAME=PROIM; NOTE=PROIM 1:74-77 (2000);
CC WWW=http://www.ncbi.nlm.nih.gov/prov/guide/204270028.g.htm".
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X80038; CA56342.1; -.
DR EMBL; AF058448; AAC23797.1; -.
DR EMBL; BC003091; AA03091.1; -.
DR EMBL; AF044968; AAC82348.1; -.
DR EMBL; AF044962; AAC82348.1; JOINED.
DR EMBL; AF044963; AAC82348.1; JOINED.
DR EMBL; AF044964; AAC82348.1; JOINED.
DR EMBL; AF044966; AAC82348.1; JOINED.
DR EMBL; AF044967; AAC82348.1; JOINED.
DR EMBL; AF050154; AAC02503.1; -.
DR PIR; I68093; I68093.
DR Genem; HGNC:9707; PVRL2.
DR MIM; 600798; -.
DR GO; GO:0005886; C:Plasma membrane; TAS.
DR GO; GO:0015026; F:Coreceptor activity; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR PROSITE; PS50835; IG_Like; 3.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; Alternative splicing.
FT SIGNAL 1
FT CHAIN 31
FT DOMAIN 32 538
FT DOMAIN 32 360
FT TRANSMEM 361 381
FT DOMAIN 382 538
FT DOMAIN 332 156
FT DOMAIN 162 256
FT DOMAIN 261 345
FT DISULFID 54 140
FT DISULFID 183 238
FT DISULFID 283 329
FT CARBOHYD 137 137
FT CARBOHYD 324 324
FT VARSPPLIC 351 479
FT SEQUENCE 538 AA; 57742 MW; 3AE4F8E92F624 CRC64;
SQ
Query Match 10.6%; Score 242.5; DB 1; Length 538;
Best local similarity 22.6%; Pred. No. 5e-10;
Matches 111; Conservative 66; Mismatches 202; Indels 113; Gaps 17;
QY 10 SCQAAAAAAPPGLRLRLLLLSAALIPGDCQNTFTKQVTVIEGEVATISQCVNKS 69
DB 2 AAAAAALPERSPTPLMLPLLL-----LLEFG-AQVAVVQLPEVRG-----QLCGT 49
QY 70 DSVLIQLNLP-----NRQTIYRDRPLKDSRF-----QLLNSS 104
DB 50 VELPCHLPVPGGLYISLVTWQRPDAIPANQVNV--AAHPKMGSPSPKPGSEKLSFVS 107

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QY 105 S-----ELKVSLTNWSISDEGRYFCQLYTDP--PDSEYTTITVIVPPNNMI 149
DB 108 AKOSTGODTEAELODATALHGLTVEDEGNYTCEFAFPFGSVRGWTWRLVIAPKN-QA 166
QY 150 DIQDFAVEGEIEIVNTAASKPATITRMFKG-NRELKKSVEEMSDMYTYSOLMK 208
DB 167 EAQKVTSSQPTTVALCISIEGRPPARISWLSLSDWEAKETQVSGLAGIVTYSRTLV 226
QY 209 VHKEDGVPIVQYEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTREGDALETC 268
DB 227 PSGRADGVATYCKEHESEFEEPALIPVTLISVRYPPEVIS-GYDDWYLGRTPA-TLSCD 284
QY 269 AIGKQVAVMTWVRVDEMPQHVLSGPNLFINLNKTDGTGRCEASNVIGRAHSDPYML 328
DB 285 VRSNPEPTGDMSTSTGTFPSAAGQSLVIAVDSLFTTTCVTYNAVGMRAEQVI 344
QY 329 VYDPEPTTIPPTTTTTTTTTTTTTTTTTTTTIDSRAGEGSIKRAVDAVIGVAVVVFAM 368
DB 345 FVRETPMT-----AGAGATGAI-----TGIITAIITAT 373
QY 369 LCLLIIGRYFARHKGYTFHEAKGADADAD-----TALINAE-----G 429
DB 374 VAATGILICROQREQT-----LQGAEDDELGGPSYKPTPKAKLEQEMPSQLFTUG 428
QY 430 GQNNSEKKEVF 441
DB 429 ASHSPKTPYF 440

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RESULT 6

PVR_HUMAN STANDARD; PRT; 417 AA.

AC P15151; P15152; Q15267; Q15268;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Poliovirus receptor precursor (CD155 antigen).
 GN PVR OR PVS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP MEDLINE=9106015; PubMed=2538245;
 RX Mendelsohn C.L., Wimmer E., Racanelli V.R.;
 RT "Cellular receptor for poliovirus: molecular cloning, nucleotide
 RT sequence, and expression of a new member of the immunoglobulin
 RT superfamily.";
 RL Cell 56:855-865(1989).
 RN [2]
 RP REVISIONS.
 RA Racanelli V.R.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RX MEDLINE=9106015; PubMed=2170108;
 RA Koike S., Horie H., Ise I., Okitsu A., Yoshida M., Iizuka N.,
 RA Takeuchi K., Takegami T., Nomoto A.;
 RT "The poliovirus receptor protein is produced both as membrane-bound
 RT and secreted forms.";
 RL EMBO J. 9:3217-3224(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Kodoyanagi V., Severin J., Ge Y., Grable L., Kvistad E., Gordon L.,
 RA Shannon M., Brower A., Olsen A.S., Smith L.M.;
 RT "Sequence analysis of a 1mb region in 19q13.2 containing a zinc finger
 RT gene cluster.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP DOMAINS.
 RX MEDLINE=91239515; PubMed=1851992;
 RA Koike S., Ise I., Nomoto A.;

RT "Functional domains of the poliovirus receptor";
Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108(1991).
RN [6]
RP MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=93059689; PubMed=1331527;
RA Zibert A., Wimmer E.;
RT "N glycosylation of the virus binding domain is not essential for
function of the human poliovirus receptor";
J. Virol. 66:7368-7373(1992).
CC -1- FUNCTION: Not known. Used by poliovirus to bind and enter the
cell.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
delta). Secreted (isoforms beta and gamma).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=PI151-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=PI151-2; Sequence=VSP_002617;
CC Name=Gamma;
CC IsoId=PI151-3; Sequence=VSP_002618, VSP_002619;
CC Name=Delta;
CC IsoId=PI151-4; Sequence=VSP_002620, VSP_002621;
CC MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR
VIRUS BINDING AND UPTAKE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD155 entry;
WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".
CC -----
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CC -----
DR EMBL; M24407; AAA36461.1; -;
DR EMBL; M24406; AAA36462.1; -;
DR EMBL; X64116; CAA45478.1; -;
DR EMBL; X64117; CAA45478.1; JOINED.
DR EMBL; X64118; CAA45478.1; JOINED.
DR EMBL; X64119; CAA45478.1; JOINED.
DR EMBL; X64120; CAA45478.1; JOINED.
DR EMBL; X64121; CAA45478.1; JOINED.
DR EMBL; X64122; CAA45478.1; JOINED.
DR EMBL; X64123; CAA45478.1; JOINED.
DR EMBL; X64116; CAA45479.1; -;
DR EMBL; X64117; CAA45479.1; JOINED.
DR EMBL; X64118; CAA45479.1; JOINED.
DR EMBL; X64119; CAA45479.1; JOINED.
DR EMBL; X64120; CAA45479.1; JOINED.
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DR EMBL; X64122; CAA45479.1; JOINED.
DR EMBL; X64123; CAA45479.1; JOINED.
DR EMBL; X64116; CAA45480.1; JOINED.
DR EMBL; X64117; CAA45480.1; JOINED.
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DR EMBL; X64119; CAA45480.1; JOINED.
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DR EMBL; X64121; CAA45480.1; JOINED.
DR EMBL; X64122; CAA45480.1; JOINED.
DR EMBL; X64123; CAA45480.1; JOINED.
DR EMBL; AC068948; AAF69803.1; -;
DR PIR; A43024; RMH0P.
DR PIR; S12048; RMH0P.
DR GENE; HGNC:9705; PVR.
DR MIM; 173850; -;
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007125; P:invasive growth; TAS.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS00835; Ig_LIKE_3.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
Repeat; Antigen; Alternative splicing; Polymorphism.
FT SIGNAL 1 20
FT CHAIN 21 417
FT DOMAIN 21 343
FT TRANSMEM 344 367
FT DOMAIN 368 417
FT DOMAIN 24 139
FT DOMAIN 145 237
FT DOMAIN 244 328
FT DISULFID 49 123
FT DISULFID 166 221
FT DISULFID 266 312
FT DISULFID 105 105
FT CARBOHYD 120 120
FT CARBOHYD 188 188
FT CARBOHYD 218 218
FT CARBOHYD 237 237
FT CARBOHYD 278 278
FT CARBOHYD 307 307
FT CARBOHYD 313 313
FT CARBOHYD 340 384
FT VARSPLIC 331 331
FT VARSPLIC 332 384
FT VARSPLIC 385 392
FT VARSPLIC 393 417
FT VARSPLIC 67 67
FT VARSPLIC 340 340
FT VARSPLIC 417 AA; 45302 MM; D15C012CE853169B CXC64;
SQ SEQUENCE 417 AA; 45302 MM; D15C012CE853169B CXC64;
Query Match 10.5%; Score 240; DB 1; Length 417;
Best Local Similarity 25.9%; Pred. No. 5.5e-10;
Matches 107; Conservative 53; Mismatches 177; Indels 76; Gaps 17;
QY 14 AAAAAAPPGRLRLLLLFSAALLIPGDCGNLFKQVTV-----IEGEVATISQ 65
2 AAAAAAPFLLLVALLVLSWP-----PQGTG-----DVVQAAPTQVPGFGDSVTLPCY 50
QY 66 V-----NKSDSVIQL-----NPNRQTIYFRDFEPLNDSRFOLLNFSSELSKSLTNVNS--- 115
51 LQVPMWETHYSQLMWAKHSGESMAVHQDQPGSYSSKLEFPAALGLMELRNASLRM 110
QY 116 ----ISDEGRYFCQDYTPDPQESYTT---ITVLPNRMIMIDIOCTAVEGESEIV-NCT 167
111 FGLRVEDENYTC-LFTVFPQGSRSVDIMLRVLAKPN-TAEVQR-VOLTEPVMARCV 167
QY 168 AAKSKPATITIRFKONTLKGSEVEW-SDVYATYTSQMLKVHKHEDDGVPIYCOVEHPA 226
168 STGGRPPACITWHSIDGKPNTSQVPGFSGVITVTSMLIIVPSSQVDEKAVTCAVEHES 227
QY 227 VTGNLQTRYLEVQYKPOVHIQMTYPLQGLTRREGDALBELTCAIKPOPVVTVVRVDE 286
228 FEKRPQLTVNLTVVYYPEVIS-GYDNMWYLGQNEA-TLTCARASNPEBTGYMSTWGP 285
QY 287 MPQHAVLSGPNLFNNKAKTDNGYRCASNIYGAHSDYMLXYVDPPTTTPPTTTTT 346
286 LPFVAQAGACOLLIRPVDKPIINTVTLICVNTNLAGRQELTVQVEGSPS----- 335
QY 347 TTTTTLTITDSRAGEGSIKRAVDHVGVAVVFAMCLLIIIGRYF 399
336 -----EHSGISR-NALIFLVGIIVF---LTLIGIYF 365

ID	PVRL_MOUSE	STANDARD;	PRT;	515 AA.
RESULT 7				
CC	SEQUENCE FROM N.A.			
CC	MEDLINE=20243787; PubMed=10781093;			
CC	Mednelli L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J.,			
CC	Leocor E., Dubreuil P., Campadelli-Fiume G.;			
CC	"The murine homolog of human nectin delta serves as a species			
CC	nonspecific mediator for entry of human and animal alpha herpesviruses			
CC	in a pathway independent of detectable binding to gD.";			
CC	Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).			
CC	[2]			
CC	SEQUENCE FROM N.A.			
CC	MEDLINE=20541977; PubMed=11090177;			
CC	Shukla P., Dal Canto M.C., Rowe C.L., Spear P.G.;			
CC	"Striking similarity of murine nectin-1alpha to human nectin-1alpha			
CC	(Hec) in sequence and activity as a glycoprotein D receptor for			
CC	alphaherpesvirus entry.";			
CC	J. Virol. 74:11773-11781(2000).			
CC	[3]			
CC	SEQUENCE FROM N.A.			
CC	STRAIN=Swiss Webster;			
CC	Zhan J., Wimmer E.;			
CC	"Mouse nectin-1 (mPR), a herpesvirus receptor, is expressed in the			
CC	floor plate during embryogenesis, suggesting a role in neural			
CC	development.";			
CC	Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR			
CC	ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO			
CC	CELLS.			
CC	-1- SUBUNIT: Interacts with HSV glycoprotein D (gD).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.			
CC	-1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; AF239762; AAF60333.1; -			
CC	EMBL; AF270977; AAF76195.1; -			
CC	EMBL; AF297665; AAG22808.1; -			
CC	MED; MG11926483; Pvr11.			
CC	GO; GO:0005913; C:cell-cell adherens junction; IDA.			
CC	GO; GO:0005515; F:protein binding; IPI.			
CC	GO; GO:004872; F:receptor activity; IDA.			
CC	InterPro; IPR007110; IG-1-like.			
CC	InterPro; IPR003599; IG.			
CC	Pfam; PF00047; IG; 2.			
CC	SMART; SM00409; IG; 2.			
CC	PROSITE; PS50835; IG_LIKE; 2.			
CC	Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;			
CC	Signal; Glycoprotein; Signal.			
CC	POTENTIAL.			
CC	POLIOVIRUS RECEPTOR RELATED PROTEIN 1.			
CC	CHAIN			
CC	1			
CC	30			
CC	515			

Query Match	Best Local Similarity	Matches	Conservative	Score	DB 1; Length	DB 1; Pred.	DB 1; No. Mismatches	DB 1; Indels	DB 1; Gaps
91	PLKSRPQLNPFSSSELKVSILTNVISIDEGKIFCOLYDPP--QESYTIIVLVPPRLM	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	PPYERKVEFELPSFIDGTIRLSGLEDEGNYICEFAFPFGNRSQNLTYMAKPTW-	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	IDICKDITAV---EGEEIEV---NCTAMASRPATTIRFMKNTTELKGSVEEW---SDM	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	IECTRAVLNARKQDNKVLVACTSANGKRPASVW---ETRLKGAELVQELRNPGT	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	YTVNSQMLKXHKEDDGPVYCOVBNHRAVNTGLQTOR---LEVQYKPOV-----	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	VTVSRKLVPSRRLHROSIACTV-----NYHIDRRESLTLNVQYEPVETIEGFDGN	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	HIQWPTPLQITREBDALLETCEAIGKPCQVMTWTVVVDDEMPQAHVLSGPNLFINN-L	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	WYLRRT-----DVKTLCKADANPRAVEYHMTLINSLPKGVBAQRITLFFRGPI	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	NKTNDNGTRCASNVIVGKAHSDWMLVYVDEPTTTPPTTTTTTTTTTTTTTTTTTDSRA	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	TYSLAGTYICATNPICIRSGOVENVNTEFPYTL-FTBE-----HGRRA	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	GEESGISAVIDHNAVGVAVVVFVPMLC---LLIILGRYFAHKGTFT-----	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	GQ-----MPTAIIIGVAGSVLVLIVVGGIIVALLRRRRHFKFDYSIKKHVYNGVYSKA	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	HEAKGA-----DDADADATAIINAEGGONNSEKKK 439	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	GIPQHPPMAQNIQYFDDSDDEKKA--SPUGSSSYEEEEE 441	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	DOMAIN 31 354	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	TRANSMEM 355 375	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	DOMAIN 376 515	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	DOMAIN 31 141	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	DOMAIN 145 243	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	DOMAIN 247 334	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	DOMAIN 446 442	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	DOMAIN 443 447	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	DISULFID 51 124	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	DISULFID 172 226	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	DISULFID 269 316	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	CARBOHYD 36 72	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	CARBOHYD 139 139	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	CARBOHYD 202 202	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	CARBOHYD 286 286	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	CARBOHYD 297 297	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	CARBOHYD 332 332	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	CONFLICT 138 138	98	98	10.5%; 24.4%;	515; 18	24.4%;	59;	142;	102;
91	CONFLICT 165 165	98	98	10.5%; 24.4%;					

[illegible]

FT	CARBOHYD	472	472	N-LINKED (GLCNAC.) (POTENTIAL)
FT	VARSPLIC	804	1049	Missing (in isoform N-CAM 140).
FT				/FTID=VSP_002589.
SO	SEQUENCE	1088 AA;	117778 MM;	62738B5B03F3E83 CRC64;
	Query Match	10.5%;	Score 239;	DB 1; Length 1088;
	Best Local Similarity	26.2%;	Pred. No. 2,2e-09;	
	Matches	89;	Conservative	62; Mismatches 147; Indels 42; Gaps 15
Oy	50	KDYVTEEGVAITSC---QVNSK---DVSQVLIN---	PNRQITTYFRDRPLKDSRFOL	95
Db	199	KDIQIVVNPPTIOAROLRVANATNMAESVLS	CDADGFPDPPEISWLKKEPIEDEB-EK	257
Oy	100	INFSSSELKVLSTNYSISDEGRYFCQLYTDP	POESYTTITVLVPPRLMIDIOKOTAVEA	159
Db	258	ISINENQSEMTIHTHEKODEAEYSC-INNOAG	ALEATILLKYARKKITTYENKRAVEL	316
Oy	160	EEIEVNCIATASKAPATTIRW-----FKGN	TELKGSVEVEMSDYVTTSQMLKYHKE	212
Db	317	DEITTLTCEA-SGDPIPSITWRATVANISSE	ATTLDGHIIVKEHTRM---SALTLDKIDQ	371
Oy	213	DSGVPPIQGVHPATNGNLCQRYVLEVQYKRC	QVCHIQTYPLQSLTRGDALETCEALGR	272
Db	372	TDSGEYFCIASNP-IGVDQAM-YHEVYAIKIR	---GPVYVTWEGNVNITCEVPAH	425
Oy	273	PCPEVMTWRYVDEDEPOH-----AVLSGP	---NLFINLNKTNGTGRCEASNIYVKAH	324
Db	426	PR-AAATWRPDQGLPPSSNFNSNIKYSGPT	SSLEVNPDSNDNGNVCNTAINTIGHFES	484
Oy	325	DYMLVYDPTTIPPTITTTTTTTTTTILITTD	SRAQ	364
Db	485	EFITVQADPPSS---PAIRKVEPYSSYTWIV	FDEPDESTGG	521
RESULT 9				
NTMRI_MOUSE				
ID	NTMRI_MOUSE	STANDARD;	PRT;	344 AA.
AC	Q99PUD;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Neurotrophin precursor.			
OS	Mus musculus (mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ICR; TISSUE=Brain;			
RT	Kim T.H., Choi S.C., Kim J., Jeon U.W., Kim K.D., Lee S.H.;			
RL	"Cloning and expression of mouse neurotrophin gene in the developing			
RL	nevous system."			
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6; TISSUE=Eye;			
RC	MEDLINE=22386257, PubMed=12477932.			
EX	Klausner R.L., Feinberg E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner R., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Stapleton L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uscin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosnak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Huijy S.W.,			
RA	Villalón D.K., Morley D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahney J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,			
RA	Bikeley R.M., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,			

FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 321 321 GPI-anchor amidated asparagine (Potential).
 FT LIPID 321 321
 SQ SEQUENCE 344 AA; 37998 MW; CBB39B53B3B24 CRC64;
 Query Match 10.1%; Score 230; DB 1; Length 344;
 Best Local Similarity 26.2%; Pred. No. 2.2e-09;
 Matches 84; Conservative 53; Mismatches 137; Indels 46; Gaps 14;
 Db 29 LLLLSAALIPFGDGNLFTR--DVTVEGEVATISQVKNKSDSVIQLNPNRQTI-84
 19 LRLFLVPTGVPRSGATPFKAMDNVTVRQGESATLRTCT--DNKVRVAMLNSTIL 75
 QY 85 YFRDFRPLKDSRFQNLNFSSELEKSLTNVSISSDEGRFCQLYTD-PPQESYTTITVLP 143
 76 YAGNDKMCILDPVRVLLSNTQVSIETIQNVAVDEGPTCSVQTDNHPKTSRVHLIVQS 135
 Db 144 PNLMTIDIOKDTAV-EGEEIEVNCTAMASKPATITIRFKNTLKGSEVEWSDMYVT 202
 136 PK--IVEISSDISINBGNISLTCTA-TGRPEPTVTRHISPKAVGVSEDEYLEIQGIT 192
 QY 203 SOLMLKVH--KEDDGVPIQVHEPVAVTGNLCTQRYLEYQYKPVHIOMTYPLQGL-TR 258
 193 REGSGEYECASANDVAAPVVRVNV-----VTNVPYIS-----EAKGTVP 234
 QY 259 EGDALETLCEALGKQPVMTVVRVDEMPQ-----HVLSGENLFINLNKTDNG 309
 235 VQKGTGLOCEASAVPS-AEQWFQDKRLVEGKGVKVENRPLSKLTFNVSEHDYGY 291
 Db 310 TYRCEASNIYKASHDYMLY 329
 292 NYTVASNKLGHTVASIMLF 311
 Db
 RESULT 11
 NTRI HUMAN STANDARD; PRT; 344 AA.
 ID NTRI HUMAN
 AC O9P121
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neurocrinin precursor (hnt).
 GN NT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CX NCBL_Taxid=9606;
 RN NCBL_Taxid=9606;
 RP SEQUENCE FROM N.A.
 RA Li G., Jin X., Tan X., Hu S., Yuan J., Qiang B.;
 RT "Cloning and identification of human neurocrinin full length cDNA";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Neural cell adhesion molecule.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. IgION family.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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 CC
 DR EMBL; AF126426; AAF37591.1; -
 DR MIM; 607938; -
 DR GO; GO:0008038; P:neural cell recognition; TAS.

DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00408; IGC2; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
 KW Repeat; Signal; Lipoprotein.
 FT SIGNAL 1 31
 FT CHAIN 32 31
 FT PROPEP 322 344
 FT DOMAIN 39 126
 FT DOMAIN 136 218
 FT DOMAIN 222 309
 FT DISULFID 57 115
 FT DISULFID 157 201
 FT DISULFID 243 295
 FT CARBOHYD 44 44
 FT CARBOHYD 70 70
 FT CARBOHYD 152 152
 FT CARBOHYD 284 284
 FT CARBOHYD 292 292
 FT CARBOHYD 305 305
 FT CARBOHYD 321 321
 FT LIPID 321 321
 SQ SEQUENCE 344 AA; 37971 MW; DA4D12C295ABBE3A CRC64;
 Query Match 10.0%; Score 228; DB 1; Length 344;
 Best Local Similarity 26.4%; Pred. No. 3.1e-09;
 Matches 84; Conservative 54; Mismatches 136; Indels 42; Gaps 14;
 Db 29 LLLLSAALIPFGDGNLFTR--DVTVEGEVATISQVKNKSDSVIQLNPNRQTI-84
 19 LRLFLVPTGVPRSGATPFKAMDNVTVRQGESATLRTCT--DNKVRVAMLNSTIL 75
 QY 85 YFRDFRPLKDSRFQNLNFSSELEKSLTNVSISSDEGRFCQLYTD-PPQESYTTITVLP 143
 76 YAGNDKMCILDPVRVLLSNTQVSIETIQNVAVDEGPTCSVQTDNHPKTSRVHLIVQS 135
 Db 144 PNLMTIDIOKDTAV-EGEEIEVNCTAMASKPATITIRFKNTLKGSEVEWSDMYVT 202
 136 PK--IVEISSDISINBGNISLTCTA-TGRPEPTVTRHISPKAVGVSEDEYLEIQGIT 192
 QY 203 SOLMLKVH--KEDDGVPIQVHEPVAVTGNLCTQRYLEYQYKPVHIOMTYPLQGL-TR 258
 193 REGSGEYECASANDVAAPVVRVNV-----VTNVPYIS-----EAKGTVP 234
 QY 259 EGDALETLCEALGKQPVMTVVRVDEMPQ-----HVLSGP--NLFINLNKTDNGTY 311
 235 VQKGTGLOCEASAVPS-AEQWFQDKRLVEGKGVKVENRPLSKLTFNVSEHDYGY 293
 Db 312 RCEASNIYKASHDYMLY 329
 294 TVASNKLGHTVASIMLF 311
 Db
 RESULT 12
 NC2 MOUSE STANDARD; PRT; 837 AA.
 ID NC2 MOUSE
 AC O35136; O35962;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell adhesion molecule) (F4B12).
 GN NCAM2 OR CCAM OR RNCAM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 CX NCBL_Taxid=10090;
 RN NCBL_Taxid=10090;
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RC STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium;

FT	CARBOHYD	416	406	N-LINKED (GLCNAC...)	(POTENTIAL).
FT	CARBOHYD	419	419	N-LINKED (GLCNAC...)	(POTENTIAL).
FT	CARBOHYD	445	445	N-LINKED (GLCNAC...)	(POTENTIAL).
FT	CARBOHYD	474	474	N-LINKED (GLCNAC...)	(POTENTIAL).
FT	CARBOHYD	562	562	N-LINKED (GLCNAC...)	(POTENTIAL).
FT	VARSPLIC	694	837	TLFNGELGAIIGVGNVALLLIVTVDSQCFPIRQCGLMNC	
FT				ITRMCKKSGSKSKELEGRNAYIKDSDKREIVYMRTE	
FT				DERLTINHGDSPVNEPTETPLPEKPLPKIEENGKVLVA	
FT				ETIRIKESNDIIQSEKDIDKA~> NCCENKNGNGQSVMH	
FT				LNAVGFVFVTMSISCLF (In isoform short).	
FT				/PrtId=VSP_002590.	
SQ	SEQUENCE	837 AA;	93203 MW;	70473B053A2D65AS CRC64;	
	Query Match	9.8%;	Score 223.5;	DB 1;	Length 837;
	Best Local Similarity	27.9%;	Pred. No. 2e+08;		
	Matches	92;	Conservative 52;	Mismatches 111;	Indels 75; Gaps 20;
Oy	49 TKDVTVI-----	EGEVAITSCQNKSDSDSVITQLNNRCQTTPRDF	89		
Db	102 TQEAATVLEIYOKLTFREVVSPOEFKGGDEAEVVCRRSSPADAVSWLYNHEEV-----	155			
Oy	90 RFLADSFFOLINFSSSELAKSLTNVISIDEGRYFCQULYTPPOE-SYTTITVL-VPPRN	146			
Db	156 TTIDNFPAVL----ANNQILNINSDDSIGYRCESRVARGRIDPRDIIVNPAPAI	211			
Oy	147 LMDIQD---TAVEGEIEVNCTANASKPATITIMFKGTTELKGSEVEZMSDMTV--	201			
Db	212 MM--PQSFNAIYERGEEMTLTCASGS-PDPITISWR-----NGKL-IEE-NEXYLKG	261			
Oy	202 -TSQMVKMKHEDDGVPVICOVHPATGNLQORVYLEVOYKRPVHMOMTYPIQGLTRREG	260			
Db	262 SNTLIYLRNIINKDGSYYCANKKA--GEDQQAIFLVGVQHRI-LQKR--NETTSEN	315			
Oy	261 DALETLCFAIGKPQPVWWTWVRV-----DDEMP-----QHAVLSGPMLFINNLN	304			
Db	316 GHVTLVCEAGEBPV-EITWKRAIDGMVFSEGKSPDGRILEVGQHORSS--LHIRDVK	371			
Oy	305 KTDNGTRCF-AANIYGAHSIDMYLYDP	333			
Db	372 LSDSGRYDCAPASRIQGHQRSMHLDIRAP	401			
	RESULT 13				
	NCA2_XENLA				
ID	NCA2_XENLA	STANDARD;	PRT;	1092 AA.	
AC	P36335,				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Neural cell adhesion molecule 2, 180 kDa isoform precursor (N-CAM				
DE	180).				
GN	NCA2.				
OC	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;				
OC	Xenopodinae; Xenopus.				
OX	NCBI_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=93273239; PubMed=7684721;				
RX	Torissen K.F., Krieg P.A.;				
RT	"Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus				
RT	laevis are expressed during development and in adult tissues."				
RL	Gene 127:243-247(1993).				
CC	-!- FUNCTION: This protein is a cell adhesion molecule involved in				
CC	neuron-neuron adhesion, neurite fasciculation, outgrowth of				
CC	neurites, etc.				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-!- ALTERNATIVE PRODUCTS:				
CC	Event-Alternative splicing: Named isoforms=1;				
CC	Comment=A number of isoforms are produced;				
CC	Name=1;				
CC	IsoId=E36335-1; Sequence=Displayed;				

```

CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; M76710; AAA49910.1; -.
DR PIR; JN0635; JN0635.
DR HSP; P56276; TLK.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGc2; 4.
DR PROSITE; PS50835; IG_LIKE; 5.
DR Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing; Signal.
FT SIGNAL
FT CHAIN
FT 1
FT 20 1092
FT 20 705
FT TRANSMEM 706 723
FT DOMAIN 724 1092
FT 20 108
FT 113 202
FT DOMAIN 208 295
FT 303 397
FT 400 489
FT 512 589
FT 618 686
FT 149 153
FT 158 162
FT 41 93
FT DISULFID 136 186
FT DISULFID 232 282
FT DISULFID 323 379
FT DISULFID 420 473
FT CARBOHYD 82 473
FT CARBOHYD 219 219
FT CARBOHYD 310 310
FT CARBOHYD 341 341
FT CARBOHYD 417 417
FT CARBOHYD 443 443
FT CARBOHYD 472 472
SQ SEQUENCE 1092 AA; 118062 MW; 118062 MW; CD336E058B7AD1 CRC64;

Query Match 9.8%; Score 223; DB 1; Length 1092;
Best Local Similarity 24.2%; Pred. No. 3,1e-08;
Matches 82; Conservative 67; Mismatches 150; Indels 40; Gaps 15;

```

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QY 274 CPWTVTWVVDDEMPQH-----AVLSGP--NLFINKTKDNGTYRCEASNIYKASD 325
DB 427 S-AASVWRDGLLSSNFSNKNKINGPTFSSLEVPNSDENDFGYNNCSAVNSIGHSSE 485
QY 326 YMLVYVDEPTTIPPTTTTTTTTTTTTTLTIIDSRAG 364
DB 486 FIVQADTPSS--PAIRKVEPSTWIVFDEPDATGG 521

RESULT 14
NCM2_HUMAN STANDARD; PRT; 837 AA.
ID NCM2_HUMAN
AC 015394;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2).
GN NCM2 OR NCM21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97369930; PubMed=9226371;
RA Paoloni-Giacchino A., Chen H., Antonarakis S.E.;
RT "Cloning of a novel human neural cell adhesion molecule gene (NCAM2)
RT that maps to chromosome region 21q21 and is potentially involved in
RT Down syndrome.";
RL Genomets 43:43-51(1997).
RN [2]
RC CARBOHYDRATE-LINKAGE SITES ASN-445 AND ASN-562.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666(2003).
CC -1- FUNCTION: May play important roles in selective fasciculation and
CC zone-to-zone projection of the primary olfactory axons.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed most strongly in adult and fetal
CC brain.
CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U75330; AAB80803.1; -.
DR Genew; HGNC:7657; NCM2.
DR MIM; 602040; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0007158; P:neuronal cell adhesion; TAS.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGc2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW Immunoglobulin domain; Signal.
FT SIGNAL
FT 1
FT 19
FT POTENTIAL.

```

FT CHAIN 20 837 NEURAL CELL ADHESION MOLECULE 2.
 FT DOMAIN 20 697 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 698 718 POTENTIAL.
 FT DOMAIN 719 837 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 21 108 IG-LIKE C2-TYPE 1.
 FT DOMAIN 113 202 IG-LIKE C2-TYPE 2.
 FT DOMAIN 208 297 IG-LIKE C2-TYPE 3.
 FT DOMAIN 302 396 IG-LIKE C2-TYPE 4.
 FT DOMAIN 401 491 IG-LIKE C2-TYPE 5.
 FT DOMAIN 482 581 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 594 678 FIBRONECTIN TYPE-III 2.
 FT DISULFID 42 93 PROBABLE.
 FT DISULFID 136 186 PROBABLE.
 FT DISULFID 232 281 PROBABLE.
 FT DISULFID 322 380 PROBABLE.
 FT DISULFID 422 475 PROBABLE.
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 474 474 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 837 AA; 92932 MM; C3D034106C5741C1 CRC64;

Query Match 9.7%; Score 222; DB 1; Length 837;
 Best Local Similarity 24.1%; Match No. 2.6e-08;
 Matches 120; Conservative 70; Mismatches 172; Indels 136; Gaps 28;

QY 49 TKDVTI-----EGEVATISQVNSDSVIGLNPNTQIYFRDF 89
 DB 102 TQETVVLITFYOKLTFREVVSPQFGEDAEVVCVSSAPAVASMLVHNEEV----- 155
 QY 90 RPLKDSFQNLNSSLKXSLTNVSTSDSGRYFCQLYTDPPE-SYTTITVL--VPERN 146
 DB 156 TTISDNLAWL-----ANNLQIILNINSDGIRYCGRVAREGEIDFRDIYLVNYPFI 211
 QY 147 LMTIDQKD---TAVEGEIEVNCTAMASKPATIRPFKNTLKGSEVEWSDMTV-- 201
 DB 212 SM-PQKSPNATLBERGEMTFSCRAGSS-PEPAISWFR-----NGKL-IEE-NEKYLKG 261
 QY 202 -TSQMLAKVKKEDDVAVICQVHPAVTGNLQTORLEIYQKQVHIQMTYPLQGLTRBG 260
 DB 262 SNELTYRNINSDGGYVCRANKKA--GEDEKQALQVFOPHI-IQKL--NETTYEN 315
 QY 261 DALELTCEATGKPOPVWTVWR--VD-----DEMF-----OHAIVSGNLFNNLN 304
 DB 316 GQVTLVGDABGEPIP-EITWKAVDGFTPEGDKSIDGRLEVKGQH---GSSSLHKDVX 371
 QY 305 KTDNGYRGE-ASNIYGAHSDMYLVY-----DPTT 336
 DB 372 LSGSGRYDCBAASRIGCHQKSMYLDIEYAPKFIISNOTIYSWEGNPINISCDVKSVPFAS 431
 QY 337 I-----PPTTTTTTTTTTTTTTTTTITTSRAGEEG--SIRAVDAVIGVAVAVV 385
 DB 432 IHWRRDKVLPAKNTNMLKTYSTGRKVIETAPTSNDGRVYCTKTNH--IGTRPOEIT 489
 QY 386 FAMLCT-----LLIGRYFAR-----HKGYFTHEAKGADDAADATTAIINAG 429
 DB 490 LALADVSPSYGVKIIELSTAKVSNKDSHGVPVHHYQVDAVEASE-IWKIVRSHG 549
 QY 430 GQ-----NNESEKKEFYI 442
 DB 550 VQTMVAVLNLEPNTTYEI 567

RESULT 15
 NPHN MOUSE STANDARD; PRT; 1242 AA.
 AC Q96ZS7; 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 GN Nephritin precursor (renal glomerulus-specific cell adhesion receptor).
 DE NPHS1 OR NPHN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NX NCBI_Taxid=10090.
 RN (1)
 RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
 RX MEDLINE=99436348; PubMed=10504499;
 RA Holzman L.B., St John P.L., Kovari I.A., Verma R., Holtzoefer H.,
 RA Abrahamson D.R.;
 RT "Nephritin localizes to the slit pore of the glomerular epithelial
 RT cell." Int. 56:1481-1491(1999).
 RL Kidney Int. 56:1481-1491(1999).
 RN (2)
 RP INTERACTION WITH CD2AP.
 RX MEDLINE=21590051; PubMed=11733379;
 RA Shih N.Y., Li J., Cotran R., Mundel P., Miner J.H., Shaw A.S.;
 RT "CD2AP localizes to the slit diaphragm and binds to nephrin via a
 RT novel C-terminal domain." J.
 RL Am. J. Pathol. 159:2303-2308(2001).
 RN (3)
 RP INTERACTION WITH CD2AP AND NPHS2.
 RX MEDLINE=21590460; PubMed=11733557;
 RA Schwarz K., Simons M., Reiser J., Saleem M.A., Paul C., Kriz W.,
 RA Shaw A.S., Holzman L.B., Mundel P.;
 RT "Podocin, a raft-associated component of the glomerular slit
 RT diaphragm, interacts with CD2AP and nephrin." J.
 RL Clin. Invest. 108:1621-1629(2001).
 CC - FUNCTION: Seems to play a role in the development or function of
 CC the kidney glomerular filtration barrier. May anchor the podocyte
 CC slit diaphragm to the actin cytoskeleton.
 CC - SUBUNIT: Interacts with podocin/NPHS2 and with CD2AP C-terminal
 CC domain.
 CC - SUBCELLULAR LOCATION: Type I membrane protein (potential). Located
 CC at podocyte slit diaphragm between podocyte foot processes.
 CC - TISSUE SPECIFICITY: Expressed in kidney glomeruli.
 CC - PTM: Phosphorylated on tyrosine residues (By similarity).
 CC - SIMILARITY: Belongs to the immunoglobulin superfamily.
 CC - SIMILARITY: Contains 8 immunoglobulin-like domains.
 CC - SIMILARITY: Contains 1 fibronectin type III domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF168466; AAF03368.1; .
 CC MGD; MGI:1859637; Nphs1.
 CC GO; GO:0005515; F:protein binding; IPI.
 CC GO; GO:0007254; P:JNK cascade; IDA.
 CC GO; GO:0000165; P:MAPKK cascade; IDA.
 CC InterPro; IPR008957; FN_III-like.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003598; Ig_c2.
 CC Pfam; PF00041; fn3.1.
 CC Pfam; PF00047; Ig.8.
 CC SMART; SM00060; FN3.1.
 CC SMART; SM00408; IGc2.1.
 CC PROSITE; PS00835; Ig-LIKE.8.
 CC Cell adhesion; Transmembrane; Signal; Glycoprotein;
 CC Immunoglobulin domain; Repeat; Phosphorylation.
 CC SIGNAL 1 22
 FT CHAIN 23 1242 NEPHRIN.
 FT DOMAIN 23 1064 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1065 1086 POTENTIAL.
 FT DOMAIN 1087 1242 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 1242 130 IG-LIKE C2-TYPE 1.

```
FT DOMAIN 135 233 IG-LIKE C2-TYPE 2.
FT DOMAIN 242 333 IG-LIKE C2-TYPE 3.
FT DOMAIN 340 434 IG-LIKE C2-TYPE 4.
FT DOMAIN 440 540 IG-LIKE C2-TYPE 5.
FT DOMAIN 544 635 IG-LIKE C2-TYPE 6.
FT DOMAIN 740 832 IG-LIKE C2-TYPE 7.
FT DOMAIN 838 939 IG-LIKE C2-TYPE 8.
FT DOMAIN 941 1025 FIBRONECTIN TYPE-III.
FT DISULFID 53 111 POTENTIAL.
FT DISULFID 160 217 POTENTIAL.
FT DISULFID 265 317 POTENTIAL.
FT DISULFID 361 417 POTENTIAL.
FT DISULFID 465 528 POTENTIAL.
FT DISULFID 567 623 POTENTIAL.
FT DISULFID 761 816 POTENTIAL.
FT DISULFID 863 920 POTENTIAL.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 547 547 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 680 680 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 708 708 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 908 908 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1242 AA; 134890 MW; 02D82180BF145092 CRC64;
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Query Match

9.7% Score 222; DB 1; Length 1242;

Best Local Similarity 23.0%; Pred. No. 4,3e-08; Matches 87; Conservative 74; Mismatches 164; Indels 54; Gaps 16;

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QY 23 GLRLRLLLLSAALLPTGDSQN-----LFTKDYVIEGEVATISQVNSKSD 71
DB 4 GTTRASLL--AGMLTTGLAQSPVTSAPRGFWALSENLTVEGSTIKLMQGV-RAPG 59
QY 72 SVVQ-----LNNRQRTYFRDRPLKDSRFPQLNFSSELKVSLTNVSISDEGRYFCQ 125
DB 60 SVVQWADGILLGNPKIPGFPKYSLEGDS-----AKGEFHLLIACDLSDDAEYECQ 112
QY 126 LYTD--PQ--ESYTTITVLPENLMIDIKD---TAVEGEIEVNCNAMASKPATIR 178
DB 113 VGRSELGPELVSPRIVLSVLPKVLQLTPEAGSTVTWAGQEVVTVCSGAKPAPDII 172
QY 179 WFKGNTELKG-KSEVEWMSD--MYTVISQMLKYNHKKEDGVPVICOVEHRAVNGNLTQR 235
DB 173 FIQGRTEVEDVSSSVNSESSEKLFTEAEARVTPQSSDNGQLVCEGSNPAALPPIKASF 232
QY 236 YLEVOYKPKQVHIQMTVP--LOGLTREGDALELTCEAIGKPPQVWTVWVRVDEM----P 288
DB 233 TMMNLFPFGPPV-IDWGLNGEHRAGENLELPCIRAGNPPATLQWLKNGKXPVSIAMGT 291
QY 289 QHAVLGGNLFINNLTNDNGT-YRCAASNTVGKHSQVMLVYVDPTTIPPTT-----P 343
DB 292 EHAQAVASHVLMVTRPEDHGARLSCOSYNSVSAETQERSITL---QVTRPPSAVITLGS 348
QY 344 TTTTTLTTLTTLTTLTDR 362
DB 349 TSQSENKAVTLCCLTKSSR 367
```

Search completed: July 7, 2004, 06:03:53
Job time : 30.126 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 ; Search time 61.8289 Seconds

(without alignments)
2255.564 Million cell updates/sec

Title: US-10-622-237-2

Perfect score: 2283
Sequence: 1 MASVVLPSGSGCAAAAAA.....AIIINAGGQNSEKEKYEPI 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2280	99.9	442	4	Q9BY67
2	2241.5	98.2	445	11	Q8R4L1
3	2232.5	97.8	445	11	Q8K3T6
4	2221	97.3	456	11	Q8R5M8
5	2134.5	93.5	443	4	Q8N2F4
6	2071.5	90.7	417	11	Q7TNU1
7	1715	75.1	333	4	Q86WB8
8	1683.5	73.7	336	11	Q80VG4
9	1671.5	73.2	336	11	Q9DEB7
10	1526	66.8	295	11	Q9Z2H8
11	1503.5	65.0	306	11	Q9QYL6
12	1483	65.0	295	11	Q9QYL6
13	1394	61.1	289	11	Q9QYL6
14	1370.5	60.0	278	11	Q9QYL3
15	903	39.6	435	4	Q8N3J6
16	893	39.1	437	4	Q81ZP8

17	863	37.8	395	11	Q8BXJ7	Q8BXJ7 mus musculus
18	862.5	37.8	404	11	Q8BLQ9	Q8BLQ9 mus musculus
19	860	37.7	395	11	Q8BZP4	Q8BZP4 mus musculus
20	858.5	37.6	404	11	Q8BYP1	Q8BYP1 mus musculus
21	802	35.1	394	13	Q7ZXX1	Q7ZXX1 xenopus lae
22	767	33.6	388	4	Q8NFF28	Q8NFF28 homo sapien
23	758	33.2	388	11	Q8R464	Q8R464 mus musculus
24	744.5	32.6	396	11	Q9N28	Q9N28 mus musculus
25	739	32.4	398	4	Q8N126	Q8N126 homo sapien
26	732.5	32.1	381	4	Q9Y4A4	Q9Y4A4 homo sapien
27	722	31.6	432	4	Q9UUP1	Q9UUP1 homo sapien
28	379.5	16.6	163	11	Q8K1H8	Q8K1H8 mus musculus
29	370.5	16.2	163	4	Q8NVJ5	Q8NVJ5 homo sapien
30	368.5	16.1	152	11	Q8BS08	Q8BS08 mus musculus
31	341.5	15.0	549	11	Q9D006	Q9D006 mus musculus
32	338.5	14.8	549	11	Q9JUB9	Q9JUB9 mus musculus
33	335.5	14.7	549	4	Q8N0S3	Q8N0S3 homo sapien
34	325.5	14.3	234	4	Q81Z09	Q81Z09 homo sapien
35	316.5	13.9	438	11	Q9JUB7	Q9JUB7 mus musculus
36	316.5	13.9	510	11	Q9JUB8	Q9JUB8 mus musculus
37	287	12.6	439	13	Q57349	Q57349 gallus gall
38	268	11.7	407	4	Q9Y412	Q9Y412 homo sapien
39	265	11.6	1482	5	Q9V4Y0	Q9V4Y0 drosophila
40	263.5	11.5	5175	5	Q810L3	Q810L3 caenorhabdi
41	263.5	11.5	5198	5	Q76518	Q76518 caenorhabdi
42	261.5	11.5	510	4	Q96NY8	Q96NY8 homo sapien
43	261.5	11.5	510	4	Q8K15	Q8K15 homo sapien
44	254.5	11.1	400	6	Q8HY16	Q8HY16 cebus apell
45	247.5	10.8	530	11	Q80XJ5	Q80XJ5 mus musculus

ALIGNMENTS

RESULT 1
ID Q9BY67 PRELIMINARY; PRT; 442 AA.

AC Q9BY67;
DT 01-JUN-2001 (TRMBLrel. 17, Created)
DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
DE Necitin-like protein 2.
GN NEC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
RT "Cloning of a novel human cDNA encoding a member of the immunoglobulin superfamily.";
RT Submitted (Mar-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL, AF132811; AAF69029.1; --
DR GeneW; HGNC:5951; IG8F4.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00047; IG_3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IG2; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 442 AA; 48537 MW; 6818353238735062 CRC64;

Query Match 99.9%; Score 2280; DB 4; Length 442;
Best Local Similarity 99.8%; Pred. No. 1.4e-16;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVVLPSGSGCAAAAAAAPPGLRLRLILLIFSAALIFPTGQONTFTKQVTVIEGEVA 60
1 MASVVLPSGSGCAAAAAAAPPGLRLRLILLIFSAALIFPTGQONTFTKQVTVIEGEVA 60
Db

QY 61 TISCOVVKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQOLNFSSELKVSILNVSISDEG 120
DB 61 TISCOVVKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQOLNFSSELKVSILNVSISDEG 120
QY 121 RYFCQVLTDPDQESYTTITVLVPPRNLMDIQDCTAVEGEIEVNTCTAMASKPATITIRF 180
DB 121 RYFCQVLTDPDQESYTTITVLVPPRNLMDIQDCTAVEGEIEVNTCTAMASKPATITIRF 180
QY 181 KGNTELKGSKEVEEWSMDYTVTSQMLKVHKEDDGVVICOVEHPAVTGNLQTORYLEVQ 240
DB 181 KGNTELKGSKEVEEWSMDYTVTSQMLKVHKEDDGVVICOVEHPAVTGNLQTORYLEVQ 240
QY 241 YKQVHIQMTYPIQGLTREGDALELTCEAIGKQPMVWTVVRVDDMPQHAVLSGPNLFI 300
DB 241 YKQVHIQMTYPIQGLTREGDALELTCEAIGKQPMVWTVVRVDDMPQHAVLSGPNLFI 300
QY 301 NNINKTNDNGTGRCAASNVGKASHDYMLYYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
DB 301 NNINKTNDNGTGRCAASNVGKASHDYMLYYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEEGSIRAVDHAIVIGVAVVFPMLCLLIIIGRYFARHKGYFTHEAKGADDA 420
DB 361 SRAGEEGSIRAVDHAIVIGVAVVFPMLCLLIIIGRYFARHKGYFTHEAKGADDA 420
QY 421 DTAIINAEQGNSEKKEEYFI 442
DB 421 DTAIINAEQGNSEKKEEYFI 442

RESULT 2

Q8R4L1 PRELIMINARY; PRT; 445 AA.
ID Q8R4L1
AC Q8R4L1
DT 01-JUN-2002 (TIEMBLrel. 21, Created)
DT 01-JUN-2002 (TIEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TIEMBLrel. 25, Last annotation update)
DE Tumor suppressor in lung cancer 1.
GN IGSF4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Fukami T., Maruyama T., Murakami Y.;
RT "Identification of murine orthologue of the TSL1 gene."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF434663; ALU6736.1; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0080021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
DR GO; GO:0005515; F:protein binding; IPT.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; Ig_3.
DR SMART; SM00408; IgC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 445 AA; 48664 MW; C5DSA070DAF70B55 CRC64;

Query Match 98.2%; Score 2241.5; DB 11; Length 445;
Best Local Similarity 98.0%; Pred. No. 2.8e-183;
Matches 436; Conservative 1; Mismatches 5; Indels 3; Gaps 1;
QY 1 MASVILPSGSGCAAA--AAAAAPGRLRLILLILFSAAALIFPTGQNLFTKDVTVIEG 57
DB 1 MASVILPSGSGCAAA--AAAAAPGRLRLILLILFSAAALIFPTGQNLFTKDVTVIEG 60

QY 58 EVATISCOVVKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQOLNFSSELKVSILNVSIS 117
DB 61 EVATISCOVVKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQOLNFSSELKVSILNVSIS 120
QY 118 DEGRYFCQVLTDPDQESYTTITVLVPPRNLMDIQDCTAVEGEIEVNTCTAMASKPATIT 177
DB 121 DEGRYFCQVLTDPDQESYTTITVLVPPRNLMDIQDCTAVEGEIEVNTCTAMASKPATIT 180
QY 178 RWFKNTELKGSKEVEEWSMDYTVTSQMLKVHKEDDGVVICOVEHPAVTGNLQTORYL 237
DB 181 RWFKNTELKGSKEVEEWSMDYTVTSQMLKVHKEDDGVVICOVEHPAVTGNLQTORYL 240
QY 238 EVQYKQVHIQMTYPIQGLTREGDALELTCEAIGKQPMVWTVVRVDDMPQHAVLSGPN 300
DB 241 EVQYKQVHIQMTYPIQGLTREGDALELTCEAIGKQPMVWTVVRVDDMPQHAVLSGPN 300
QY 298 LFINNKLTNDNGTGRCAASNVGKASHDYMLYYDPTTIPPTTTTTTTTTTTTTTTTT 357
DB 301 LFINNKLTNDNGTGRCAASNVGKASHDYMLYYDPTTIPPTTTTTTTTTTTTTTTTT 360
QY 358 ITDSRAGEEGSIRAVDHAIVIGVAVVFPMLCLLIIIGRYFARHKGYFTHEAKGADDA 417
DB 361 ITDSRAGEEGSIRAVDHAIVIGVAVVFPMLCLLIIIGRYFARHKGYFTHEAKGADDA 420
QY 418 ADADTAIINAEQGNSEKKEEYFI 442
DB 421 ADADTAIINAEQGNSEKKEEYFI 445

RESULT 3

Q8K3T6 PRELIMINARY; PRT; 445 AA.
ID Q8K3T6
AC Q8K3T6
DT 01-OCT-2002 (TIEMBLrel. 22, Created)
DT 01-OCT-2002 (TIEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TIEMBLrel. 25, Last annotation update)
DE Synaptic cell adhesion molecule 1.
GN IGSF4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Biederer T.C., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,
RT "SynCAM, a synaptic adhesion molecule that drives synapse assembly."
RL Science 0:0-0 (2002).
DR EMBL; AF539424; AN01614.1; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0080021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
DR GO; GO:0005515; F:protein binding; IPT.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG_c2.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; Ig_3.
DR SMART; SM00408; IgC2; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 445 AA; 48666 MW; 5B336F23F1877497 CRC64;

Query Match 97.8%; Score 2232.5; DB 11; Length 445;
Best Local Similarity 97.5%; Pred. No. 1.7e-182;
Matches 434; Conservative 2; Mismatches 6; Indels 3; Gaps 1;
QY 1 MASVILPSGSGCAAA--AAAAAPGRLRLILLILFSAAALIFPTGQNLFTKDVTVIEG 57


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Db 1 MASAVLPSSGSCAAAAAAPPGLRLRLLLLLLSAALIPFGDGNLFTKDVTVIEG 60
QY 58 EVATISCCVKNKSDSDSVIGLNPNRQTIYFRDPRFLKDSRFOLNFSSELKVSILTNVSI 117
Db 61 EVATISCCVKNKSDSDSVIGLNPNRQTIYFRDPRFLKDSRFOLNFSSELKVSILTNVSI 120
QY 118 DEGRYFCQLYTDPPEOSYTTITVLVPPRNLIMIDIQKTAVEGEIEVNCCTAMASKPATTI 177
Db 121 DEGRYFCQLYTDPPEOSYTTITVLVPPRNLIMIDIQKTAVEGEIEVNCCTAMASKPATTI 180
QY 178 RWFKGNTELKGSKEVEEWSMDYVTSQMLKVKHEDDGPVICOVEHPATGNLQTORYL 237
Db 181 RWFKGNTELKGSKEVEEWSMDYVTSQMLKVKHEDDGPVICOVEHPATGNLQTORYL 240
QY 238 EVOYKPOVHIQMTYPLQGLTREGDALTELCEAIKGPQVMTWVRVDDMPQHAVLSGN 297
Db 241 EVOYKPOVHIQMTYPLQGLTREGDALTELCEAIKGPQVMTWVRVDDMPQHAVLSGN 300
QY 298 LFINNLKNTDNGTYRCEASNIYKASDYMUYVDPPTTIPPTTTTTTTTTTTTTTTTTI 357
Db 301 LFINNLKNTDNGTYRCEASNIYKASDYMUYVDPPTTIPPTTTTTTTTTTTTTTTTTI 360
QY 358 ITTSRAGEGSIKRAVDNAVIGVAVVVFAMLCILILIGRYFARHKGTFTHEAKGADDA 417
Db 361 ITTSRAGEGSIKRAVDNAVIGVAVVVFAMLCILILIGRYFARHKGTFTHEAKGADDA 420
QY 418 ADADTALINAEQGQNNSEKKEYFI 442
Db 421 ADADTALINAEQGQNNSEKKEYFI 445

RESULT 4
Q8RS58 ID Q8RS58 PRELIMINARY; PRT; 456 AA.
AC Q8RS58;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RA175.
GN IGSF4 OR RA175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Menot T.;
RT "Biological function of RA175, a new member of immunoglobulin super
RT family.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB064265; BAB83501.2; -.
DR MGD; MGI:1889272; IGSF4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . ; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003585; Neurixin-like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 456 AA; 49787 MW; 322E86644B01C7F CRC64;

```

Query Match 97.3%; Score 2221; DB 11; Length 456;
 Best Local Similarity 95.4%; Pred. No. 1,7e-181;
 Matches 435; Conservative 2; Mismatches 5; Indels 14; Gaps 2;

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QY 1 MASVLPSSGSCAAAA--AAAAAPGLRLRLLLLLLSAALIPFGDGNLFTKDVTVIEG 57
Db 1 MASAVLPSSGSCAAAAAAPPGLRLRLLLLLLSAALIPFGDGNLFTKDVTVIEG 60
QY 58 EVATISCCVKNKSDSDSVIGLNPNRQTIYFRDPRFLKDSRFOLNFSSELKVSILTNVSI 117
Db 61 EVATISCCVKNKSDSDSVIGLNPNRQTIYFRDPRFLKDSRFOLNFSSELKVSILTNVSI 120
QY 118 DEGRYFCQLYTDPPEOSYTTITVLVPPRNLIMIDIQKTAVEGEIEVNCCTAMASKPATTI 177
Db 121 DEGRYFCQLYTDPPEOSYTTITVLVPPRNLIMIDIQKTAVEGEIEVNCCTAMASKPATTI 180
QY 178 RWFKGNTELKGSKEVEEWSMDYVTSQMLKVKHEDDGPVICOVEHPATGNLQTORYL 237
Db 181 RWFKGNTELKGSKEVEEWSMDYVTSQMLKVKHEDDGPVICOVEHPATGNLQTORYL 240
QY 238 EVOYKPOVHIQMTYPLQGLTREGDALTELCEAIKGPQVMTWVRVDDMPQHAVLSGN 297
Db 241 EVOYKPOVHIQMTYPLQGLTREGDALTELCEAIKGPQVMTWVRVDDMPQHAVLSGN 300
QY 298 LFINNLKNTDNGTYRCEASNIYKASDYMUYVDPPTTIPPTTTTTTTTTTTTTTTTTI 357
Db 301 LFINNLKNTDNGTYRCEASNIYKASDYMUYVDPPTTIPPTTTTTTTTTTTTTTTTTI 360
QY 358 IT-----DSRAGEGSIKRAVDNAVIGVAVVVFAMLCILILIGRYFARHKGT 406
Db 361 ITDTTATTEPRAVHDSRAGEGSIKRAVDNAVIGVAVVVFAMLCILILIGRYFARHKGT 420
QY 407 FTHEAKGADDAADADTALINAEQGQNNSEKKEYFI 442
Db 421 FTHEAKGADDAADADTALINAEQGQNNSEKKEYFI 456

RESULT 5
Q8N2F4 ID Q8N2F4 PRELIMINARY; PRT; 443 AA.
AC Q8N2F4;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RA175.
GN IGSF4 OR RA175.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Embryo;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahara K., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075502; BC01657.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 443 AA; 48648 MW; 046B43A156F64 CRC64;

```

Query Match 93.5%; Score 2134.5; DB 4; Length 443;
 Best Local Similarity 94.4%; Pred. No. 4.1e-174;
 Matches 418; Conservative 4; Mismatches 20; Indels 1; Gaps 1;

```

Db 61 TISQVVKSDSDSVIQLNPNKQTIYFDFRPLKDSRQOLNPFSSSEIKVSLTNVSI:SDSG 120
Qy 121 RYFCQLYTDPPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCSTAMASKPATIIRMF 180
Db 121 RYFCQLYTDPPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCSTAMASKPATIIRMF 180
Qy 181 KGNTELKGSKEVEBWSMNTVTSQMLKVKHKEDGVPVTCQVHPAVTGNLQTORYLEVO 240
Db 181 KGNTELKGSKEVEBWSMNTVTSQMLKVKHKEDGVPVTCQVHPAVTGNLQTORYLEVO 240
Qy 241 YKPOVHIQMTYPIQGLTRBGDALELTCEAIGKQPPVWVTVVRVDDEMPQHAVLSGNLFT 300
Db 241 YKPOVHIQMTYPIQGLTRBGDALELTCEAIGKQPPVWVTVVRVDDEMPQHAVLSGNLFT 300
Qy 301 NNINKTDNGTYRCEASNIVGKASHDYMLVYDPTTIPPTTTTTTTTTTTT-LTIT 359
Db 301 NNINKTDNGTYRCEASNIVGKASHDYMLVYDPTTIPPTTTTTTTTTTTT-LTIT 359
Qy 360 DSRAGEGSIKRAVDHAVIGGVAVVVFAMCLIIIGRYFARKKGYTFTHKAGDAD 419
Db 361 DSRAGEGSIKRAVDHAVIGGVAVVVFAMCLIIIGRYFARKKGYTFTHKAGDAD 420
Qy 420 ADTAIINAEQGQNNSEKKEYFI 442
Db 421 ADTAIINAEQGQNNSEKKEYFI 443

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RESULT 6

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ID Q7TNLI PRELIMINARY; PRT; 417 AA.
AC Q7TNLI;
DT 01-OC2-2003 (Tremblrel. 25, Created)
DT 01-OC2-2003 (Tremblrel. 25, Last sequence update)
DT 01-OC2-2003 (Tremblrel. 25, Last annotation update)
DE Necltin-like molecule 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Shingai T., Ikeda W., Kakunaga S., Morimoto K., Takekuni K., Itoh S.,
RA Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.;
RT "Implications of necltin-like molecule
RT 2/IGSF4/BA175/SGISF/TSLC1/SYNCAM1 in cell-cell adhesion and
RT transmembrane protein localization in epithelial cells.";
RL J. Biol. Chem 0:0-0(2003).
DR EMBL: AY351388; AA02281.1;
SQ SEQUENCE 417 AA; 45779 MW; 98500180D37845C2 CRC64;

```

Query Match 90.7%; Score 2071.5; DB 11; Length 417;
 Best Local Similarity 91.7%; Pred. No. 9.2e-169;
 Matches 408; Conservative 1; Mismatches 5; Indels 31; Gaps 2;

```

Qy 1 MASVVLPSGSCQCAAA--AAAAPPGIRLRLLLLLSAALLPTGGQNLFTKDVTVIEG 57
Db 1 MASVVLPSGSCQCAAAAVAAAAPPGIRLRLLLLLSAALLPTGGQNLFTKDVTVIEG 60
Qy 58 EVATTICQVVKSDSDSVIQLNPNKQTIYFDFRPLKDSRQOLNPFSSSEIKVSLTNVSI:SDSG 117
Db 58 EVATTICQVVKSDSDSVIQLNPNKQTIYFDFRPLKDSRQOLNPFSSSEIKVSLTNVSI:SDSG 117
Qy 61 EVATTICQVVKSDSDSVIQLNPNKQTIYFDFRPLKDSRQOLNPFSSSEIKVSLTNVSI:SDSG 120
Db 61 EVATTICQVVKSDSDSVIQLNPNKQTIYFDFRPLKDSRQOLNPFSSSEIKVSLTNVSI:SDSG 120
Qy 118 DESRRYFCQLYTDPPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCSTAMASKPATIIRMF 177
Db 118 DESRRYFCQLYTDPPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCSTAMASKPATIIRMF 177
Qy 121 DEGRYFCQLYTDPPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCSTAMASKPATIIRMF 180
Db 121 DEGRYFCQLYTDPPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCSTAMASKPATIIRMF 180
Qy 178 RWFKGNTELKGSKEVEBWSMNTVTSQMLKVKHKEDGVPVTCQVHPAVTGNLQTORYLEVO 237
Db 181 RWFKGNTELKGSKEVEBWSMNTVTSQMLKVKHKEDGVPVTCQVHPAVTGNLQTORYLEVO 240
Qy 238 EVOYKPOVHIQMTYPIQGLTRBGDALELTCEAIGKQPPVWVTVVRVDDEMPQHAVLSGNLFT 297

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Db 241 EVOYKPOVHIQMTYPIQGLTRBGDALELTCEAIGKQPPVWVTVVRVDDEMPQHAVLSGNLFT 300
Qy 298 LFNNINKTDNGTYRCEASNIVGKASHDYMLVYDPTTIPPTTTTTTTTTTTTILITI 357
Db 301 LFNNINKTDNGTYRCEASNIVGKASHDYMLVYDPTTIPPTTTTTTTTTTTTILITI 357
Qy 358 ITDSRAGEGSIKRAVDHAVIGGVAVVVFAMCLIIIGRYFARKKGYTFTHKAGDAD 417
Db 358 ITDSRAGEGSIKRAVDHAVIGGVAVVVFAMCLIIIGRYFARKKGYTFTHKAGDAD 417
Qy 418 ADTAIINAEQGQNNSEKKEYFI 442
Db 418 ADTAIINAEQGQNNSEKKEYFI 442
Qy 419 ADTAIINAEQGQNNSEKKEYFI 443

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RESULT 7

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ID Q86WB8 PRELIMINARY; PRT; 333 AA.
AC Q86WB8;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OC2-2003 (Tremblrel. 25, Last annotation update)
DE Secretory isoform of TSLC-1.
GN TSLC-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RA Ito A., Koma Y., Nagano T.;
RT "Cloning of a secretory isoform of SGISF/TSLC-1."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB094146; BAC66178.1;
DR InterPro: IPR003599; IG_1like.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00047; IG_3.
DR SMART: SM00409; IG_3.
DR SMART: SM00408; IG_3.
DR PROSITE: PS00835; IG_LIKE; 3.
SQ SEQUENCE 333 AA; 36915 MW; D7C1102P46D08492 CRC64;

```

Query Match 75.1%; Score 1715; DB 4; Length 333;
 Best Local Similarity 100.0%; Pred. No. 2.2e-138;
 Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 MASVVLPSGSCQCAAAAAAAPPGRRLRLLLLSAALLPTGGQNLFTKDVTVIEGVA 60
Db 1 MASVVLPSGSCQCAAAAAAAPPGRRLRLLLLSAALLPTGGQNLFTKDVTVIEGVA 60
Qy 61 TISQVVKSDSDSVIQLNPNKQTIYFDFRPLKDSRQOLNPFSSSEIKVSLTNVSI:SDSG 120
Db 61 TISQVVKSDSDSVIQLNPNKQTIYFDFRPLKDSRQOLNPFSSSEIKVSLTNVSI:SDSG 120
Qy 121 RYFCQLYTDPPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCSTAMASKPATIIRMF 180
Db 121 RYFCQLYTDPPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCSTAMASKPATIIRMF 180
Qy 181 KGNTELKGSKEVEBWSMNTVTSQMLKVKHKEDGVPVTCQVHPAVTGNLQTORYLEVO 240
Db 181 KGNTELKGSKEVEBWSMNTVTSQMLKVKHKEDGVPVTCQVHPAVTGNLQTORYLEVO 240
Qy 241 YKPOVHIQMTYPIQGLTRBGDALELTCEAIGKQPPVWVTVVRVDDEMPQHAVLSGNLFT 300
Db 241 YKPOVHIQMTYPIQGLTRBGDALELTCEAIGKQPPVWVTVVRVDDEMPQHAVLSGNLFT 300
Qy 301 NNINKTDNGTYRCEASNIVGKASHDYMLVY 331
Db 301 NNINKTDNGTYRCEASNIVGKASHDYMLVY 331

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RESULT 8
Q80VG4 ID Q80VG4 PRELIMINARY; PRT; 336 AA.
AC Q80VG4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE A secretion form of SGISF/TSIC1.
GN SGISF/TSIC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Spleen cell-derived;
RA Ito A., Koma Y., Nagano T.;
RT "A secretion form of SGISF/TSIC1."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB092414; BA66173.1; -.
DR InterPro: IPR003599; IG_1like.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00047; IG_3.
DR SMART: SM00409; IGc2; 3.
DR SMART: SM00409; IGc2; 3.
DR PROSITE: PS50835; IG_LIKE; 3.
SQ SEQUENCE 336 AA; 37155 MW; 9EF3D8B8B5E8F72 CRC64;

Query Match
Best Local Similarity 73.7%; Score 1683.5; DB 11; Length 336;
Matches 327; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 1 MASVLPSSGSCCAAA---AAAAAPGRLRLLLLFSAALIFPTDGNLFTKDYVIEG 57
DB 1 MASVLPSSGSCCAAAVAAAAPGRLRLRLLLLSAALIFPTDGNLFTKDYVIEG 60
QY 58 EVATISQVNSKSDSDSVIQLNPNRQTYFRDPRPKDSRFQNLNFSSELKVSILTNVIS 117
DB 61 EVATISQVNSKSDSDSVIQLNPNRQTYFRDPRPKDSRFQNLNFSSELKVSILTNVIS 120
QY 118 DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVGEIEIVNCTAMASKPATTI 177
DB 121 DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVGEIEIVNCTAMASKPATTI 180
QY 178 RWFKGNTELKKGSEVEMSDMTVTTSQMLKVKHEDDGVVICQVEHPATVGNLQTORYL 237
DB 181 RWFKGNTELKKGSEVEMSDMTVTTSQMLKVKHEDDGVVICQVEHPATVGNLQTORYL 240
QY 238 EVQYKPOVHIQMTYPLQGLTRREGDALELTCEAIGKPPQVMTWVRVDEMPQHAVALSGPN 297
DB 241 EVQYKPOVHIQMTYPLQGLTRREGDALELTCEAIGKPPQVMTWVRVDEMPQHAVALSGPN 300
QY 298 LFINNLKNTDNGTYRCEASNIYGAHSDYMLVYV 331
DB 301 LFINNLKNTDNGTYRCEASNIYGAHSDYMLVYV 334

RESULT 9
Q9D6E7 ID Q9D6E7 PRELIMINARY; PRT; 336 AA.
AC Q9D6E7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 2900073G06RIK protein.
GN IGSF4 OR 2900073G06RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Aochi T., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saico T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner K., Batalov S., Cavaletto T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balasubramanian R., Barsh G.,
RA Blake J., Boffelli D., Boujunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.T., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombela P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wuyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kotsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690 (2001).
DR EMBL: AK013775; BAB28988.1; -.
DR MGI: 1889272; 198f4.
DR GO: GO:0045202; C:synaptic junction; IDA.
DR GO: GO:0008021; C:synaptic vesicle; IDA.
DR GO: GO:0016347; P:calcium-independent cell adhesion molecule . . . IDA.
DR GO: GO:0005515; P:protein binding; IPI.
DR GO: GO:0007155; P:cell adhesion; IDA.
DR GO: GO:0007416; P:synaptogenesis; IDA.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00047; IG_3.
DR SMART: SM00409; IGc2; 1.
DR PROSITE: PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 336 AA; 37157 MW; FF887FAFAEFDP120 CRC64;

Query Match
Best Local Similarity 73.2%; Score 1671.5; DB 11; Length 336;
Matches 325; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 1 MASVLPSSGSCCAAA---AAAAAPGRLRLLLLFSAALIFPTDGNLFTKDYVIEG 57
DB 1 MASVLPSSGSCCAAAVAAAAPGRLRLRLLLLSAALIFPTDGNLFTKDYVIEG 60
QY 58 EVATISQVNSKSDSDSVIQLNPNRQTYFRDPRPKDSRFQNLNFSSELKVSILTNVIS 117
DB 61 EVATISQVNSKSDSDSVIQLNPNRQTYFRDPRPKDSRFQNLNFSSELKVSILTNVIS 120
QY 118 DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVGEIEIVNCTAMASKPATTI 177
DB 121 DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVGEIEIVNCTAMASKPATTI 180
QY 178 RWFKGNTELKKGSEVEMSDMTVTTSQMLKVKHEDDGVVICQVEHPATVGNLQTORYL 237
DB 181 RWFKGNTELKKGSEVEMSDMTVTTSQMLKVKHEDDGVVICQVEHPATVGNLQTORYL 240
QY 238 EVQYKPOVHIQMTYPLQGLTRREGDALELTCEAIGKPPQVMTWVRVDEMPQHAVALSGPN 297
DB 241 EVQYKPOVHIQMTYPLQGLTRREGDALELTCEAIGKPPQVMTWVRVDEMPQHAVALSGPN 300
QY 298 LFINNLKNTDNGTYRCEASNIYGAHSDYMLVYV 331
DB 301 LFINNLKNTDNGTYRCEASNIYGAHSDYMLVYV 334

RESULT 10
Q9Z2H8 ID Q9Z2H8 PRELIMINARY; PRT; 295 AA.
AC Q9Z2H8;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)

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DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nectin-like protein 2.
 GN IGSF4 OR NECT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
 RT "Cloning of a novel cDNA encoding a member of immunosuperfamily."; Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF061260; AAC67243.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro: IPR007110; Ig_c2.
 DR InterPro: IPR003585; Ig_c2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32509 MW; 9DB9D86F6F6448 CRC64;

Query Match 66.8%; Score 1526; DB 11; Length 295;
 Best Local Similarity 98.6%; Pred. No. 2.9e-122;
 Matches 291; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 148 MIDIOKTAVEGEIEVNCCTAMASKPATIRMEKGNTELGKSEVEEMDMYVTSQML 207
 DB 1 MIDIOKTAVEGEIEVNCCTAMASKPATIRMEKGNTELGKSEVEEMDMYVTSQML 60
 QY 208 KVHKEDDGVPIQVEHPATGNLQTORYLEVOYKQVHIQMTYPIQGLTRSDALELTC 267
 DB 61 KVHKEDDGVPIQVEHPATGNLQTORYLEVOYKQVHIQMTYPIQGLTRSDALELTC 120
 QY 268 EAIKGPQVWVTVRWVDEMPQHAVLSGNPLFINLNKTDNGTYRCEASNIYKKAHSDYM 327
 DB 121 EAIKGPQVWVTVRWVDEMPQHAVLSGNPLFINLNKTDNGTYRCEASNIYKKAHSDYM 180
 QY 328 LYYDPEPTIIPPTITTT 387
 DB 181 LYYDPEPTIIPPTITTT 240
 QY 388 MLCILIIIGRYFARHKGYFTHEAKGADDAADTAIINAEQGQNNSEKKEFYI 442
 DB 241 MLCILIIIGRYFARHKGYFTHEAKGADDAADTAIINAEQGQNNSEKKEFYI 295

RESULT 11
 ID 09QYL4 PRELIMINARY; PRT; 306 AA.
 AC 09QYL4
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RA175C.
 GN IGSF4 OR RA175C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kourouku Y., Momoi M.,
 RA Momoi T.;

RT "RA175, a novel neuron specific adhesion protein."; Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB021966; BAA87916.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro: IPR007110; Ig_c2.
 DR InterPro: IPR003585; Ig_c2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 306 AA; 33522 MW; A4C37B0F23554D5 CRC64;

Query Match 65.9%; Score 1503.5; DB 11; Length 306;
 Best Local Similarity 94.8%; Pred. No. 2.5e-120;
 Matches 290; Conservative 2; Mismatches 3; Indels 11; Gaps 1;

QY 148 MIDIOKTAVEGEIEVNCCTAMASKPATIRMEKGNTELGKSEVEEMDMYVTSQML 207
 DB 1 MIDIOKTAVEGEIEVNCCTAMASKPATIRMEKGNTELGKSEVEEMDMYVTSQML 60
 QY 208 KVHKEDDGVPIQVEHPATGNLQTORYLEVOYKQVHIQMTYPIQGLTRSDALELTC 267
 DB 61 KVHKEDDGVPIQVEHPATGNLQTORYLEVOYKQVHIQMTYPIQGLTRSDALELTC 120
 QY 268 EAIKGPQVWVTVRWVDEMPQHAVLSGNPLFINLNKTDNGTYRCEASNIYKKAHSDYM 327
 DB 121 EAIKGPQVWVTVRWVDEMPQHAVLSGNPLFINLNKTDNGTYRCEASNIYKKAHSDYM 180
 QY 328 LYYDPEPTIIPPTITTT 376
 DB 181 LYYDPEPTIIPPTITTT 240
 QY 377 IGVVAVVVPMCLIIIGRYFARHKGYFTHEAKGADDAADTAIINAEQGQNNSE 436
 DB 241 IGVVAVVVPMCLIIIGRYFARHKGYFTHEAKGADDAADTAIINAEQGQNNSE 300
 QY 437 KKEYFI 442
 DB 301 KKEYFI 306

RESULT 12
 ID 09QYL6 PRELIMINARY; PRT; 295 AA.
 AC 09QYL6
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RA175A.
 GN IGSF4 OR RA175A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kourouku Y., Momoi M.,
 RA Momoi T.;

DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0007155; P:cell adhesion; IDA.
 DR GO: GO:0007416; P:synapticogenesis; IDA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam: PF00047; IG_2.
 DR SMART: SM00294; 4.1m; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS50835; IG-LIKE; 2.
 DR Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32347 MW; FDD9E8145C6B971B CRC64;

Query Match 65.0%; Score 1483; DB 11; Length 295;
 Best Local Similarity 95.9%; Pred. No. 1.4e-118;
 Matches 283; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 148 MIDIQDVAEGEIEVNCCTAMASKPATITIRWFKGNTELKSGSEVEEWSDMYTTSQML 207
 DB 1 MIDIQDVAEGEIEVNCCTAMASKPATITIRWFKGNTELKSGSEVEEWSDMYTTSQML 60
 QY 208 KHKEDDGVPIQVEHPAVTGNLTQRYLEVQYKPVHIOQTYPLQGLTREGDALELTC 267
 DB 61 KHKEDDGVPIQVEHPAVTGNLTQRYLEVQYKPVHIOQTYPLQGLTREGDALELTC 120
 QY 268 EAIKRPQVMTWVAVDEMPQHAVLSGPNLFINNLTNDGTGRCEASNIYGRASDYM 327
 DB 121 EAIKRPQVMTWVAVDEMPQHAVLSGPNLFINNLTNDGTGRCEASNIYGRASDYI 180
 QY 328 LYVDPPTTIPPTTT 387
 DB 181 LYVDPPTTIPPTTT 240
 QY 388 MLCILIIIGRYFARKGTFTFHEAKGADDAADADTAIINAGGQNNSEKKEFYI 442
 DB 241 MLCILIIIGRYFARKGTFTFHEAKGADDAADADTAIINAGGQNNSEKKEFYI 295

RESULT 13

Q9QYL5 PRELIMINARY; PRT; 289 AA.

AC Q9QYL5
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RA175B.
 GN IGSF4 OR RA175B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urase K., Mukasa T., Kourouku Y., Momoi M.,
 RA Momoi T.;
 RT "RA175, a novel neuron specific adhesion protein.";
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB021965; BAA87915.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO: GO:0045202; C:synaptic junction; IDA.
 DR GO: GO:0008021; C:synaptic vesicle; IDA.
 DR GO: GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
 DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0007155; P:cell adhesion; IDA.
 DR GO: GO:0007416; P:synapticogenesis; IDA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam: PF00047; IG_2.
 DR SMART: SM00294; 4.1m; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS50835; IG-LIKE; 2.
 KW Immunoglobulin domain.

SQ SEQUENCE 289 AA; 31811 MW; 8D1B836D0565A84 CRC64;

Query Match 61.1%; Score 1394; DB 11; Length 289;
 Best Local Similarity 91.9%; Pred. No. 5.6e-111;
 Matches 271; Conservative 3; Mismatches 15; Indels 6; Gaps 1;

QY 148 MIDIQDVAEGEIEVNCCTAMASKPATITIRWFKGNTELKSGSEVEEWSDMYTTSQML 207
 DB 1 MIDIQDVAEGEIEVNCCTAMASKPATITIRWFKGNTELKSGSEVEEWSDMYTTSQML 60
 QY 208 KHKEDDGVPIQVEHPAVTGNLTQRYLEVQYKPVHIOQTYPLQGLTREGDALELTC 267
 DB 61 KHKEDDGVPIQVEHPAVTGNLTQRYLEVQYKPVHIOQTYPLQGLTREGDALELTC 120
 QY 268 EAIKRPQVMTWVAVDEMPQHAVLSGPNLFINNLTNDGTGRCEASNIYGRASDYM 327
 DB 121 EAIKRPQVMTWVAVDEMPQHAVLSGPNLFINNLTNDGTGRCEASNIYGRASDYI 180
 QY 328 LYVDPPTTIPPTTT 387
 DB 181 LYVDPPTTIPPTTT 234
 QY 388 MLCILIIIGRYFARKGTFTFHEAKGADDAADADTAIINAGGQNNSEKKEFYI 442
 DB 235 MLCILIIIGRYFARKGTFTFHEAKGADDAADADTAIINAGGQNNSEKKEFYI 289

RESULT 14

Q9QYL3 PRELIMINARY; PRT; 278 AA.

AC Q9QYL3
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RA175N.
 GN IGSF4 OR RA175N.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urase K., Mukasa T., Kourouku Y., Momoi M.,
 RA Momoi T.;
 RT "RA175, a novel neuron specific adhesion protein.";
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB021967; BAA87917.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO: GO:0045202; C:synaptic junction; IDA.
 DR GO: GO:0008021; C:synaptic vesicle; IDA.
 DR GO: GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
 DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0007155; P:cell adhesion; IDA.
 DR GO: GO:0007416; P:synapticogenesis; IDA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam: PF00047; IG_2.
 DR SMART: SM00294; 4.1m; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS50835; IG-LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 278 AA; 30636 MW; A295FADDEA2724B04 CRC64;

Query Match 60.0%; Score 1370.5; DB 11; Length 278;
 Best Local Similarity 90.2%; Pred. No. 5.4e-109;
 Matches 266; Conservative 3; Mismatches 9; Indels 17; Gaps 1;

QY 148 MIDIQDVAEGEIEVNCCTAMASKPATITIRWFKGNTELKSGSEVEEWSDMYTTSQML 207
 DB 1 MIDIQDVAEGEIEVNCCTAMASKPATITIRWFKGNTELKSGSEVEEWSDMYTTSQML 60
 QY 208 KHKEDDGVPIQVEHPAVTGNLTQRYLEVQYKPVHIOQTYPLQGLTREGDALELTC 267

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Db 61 KKHEDDGVPIQVVERPATGNLQTORYLEVOYKPOVHIQMTYPIQGLTREGDALFLTC 120
Qy 268 EAIKRPQPVMTVTRVVDENPQHAVALSGPNLFNNLNTKDTNGTYRCEASNIYKASADYM 327
Db 121 EAIKRPQPVMTVTRVVDENPQHAVALSGPNLFNNLNTKDTNGTYRCEASNIYKASADYI 180
Qy 328 LYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 387
Db 181 LYVD-----TTATTEPAVHDSRAGEEGTIGAVDHAYIGVAVAVVFA 223
Qy 388 MLCILIIIGRYFAHKGTYFTHEAKGADDAADATATINAEQGQNNSEKKEYFI 442
Db 224 MLCILIIIGRYFAHKGTYFTHEAKGADDAADATATINAEQGQNNSEKKEYFI 278
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RESULT 15

```
Q8N3J6 PRELIMINARY; PRT; 435 AA.
ID Q8N3J6
AC Q8N3J6;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DE 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKFZP761G128.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amalgama;
RA Koehler K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834270; CAD38945.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 435 AA; 47554 MW; 59DD41B7F34D446 CRC64;
```

Query Match 39.6%; Score 903; DB 4; Length 435;
Best Local Similarity 44.4%; Pred. No. 1.1e-68;
Matches 193; Conservative 76; Mismatches 138; Indels 28; Gaps 7;

```
Qy 29 LLLLESAALIPFG-DGQNLFTKDYVIEGEVATISGVNKSDDSVIOLINPQOTYFR 87
Db 8 VLAFFYVCGILLQSGQGFPLTQNTVVEGGTALITCRVDQNDNTSLQNSNPAQOTLYFD 67
Qy 88 DFRPLKDSRFPQLINFSSSELKVALTNVSIISDEGRYFCQLYDPQESYTTITVLVPRNL 147
Db 68 DKKALRDNRLELFRASHEHLSISVDYSLDEGQYCSLFTWPKTSKAYLITVLGVPEKP 127
Qy 148 MIDIQDTAVGESEIIVNCTAMASKPATITRWEKSTELKGSVEVENS--DMYVTSQ 204
Db 128 QISGFSPVMEGLMQLTCTSGSKPAADIRFKNDEXIKDYKYLKEEDANKRTFTVST 187
Qy 205 LMLKVKEDDGVFVICOVEHPAVTGNLQ-TORYLEVOYKPOVHIQMTYPIQGLTREGDAL 263
Db 188 LDFRVDRSDGVAVICRVDSHSLNATPQVAMQVLEIHYTPSVKI--IPSTFPQEGQPL 244
Qy 264 ELTCEAIGKRPQPVMTVTRVVDENPQHAVALSGPNLFNNLNTKDTNGTYRCEASNIYK 321
Db 245 ILTCESKGKPLPEPVMTKDGELPDPDRKVVSGRELNLFLNKTNDNGTYRCEANTNIGQ 304
Qy 322 AHSYMLYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 367
Db 305 SSAEYVLIVHDVNTLITPTIIPSLTATVTTTVALTPTTSATTSSIRDPNALAQNG 364
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Qy 368 SIRAVDHVIGVAVVVFAMLCILIIIGRYFAHKGTYFTHEAKGADDAADATATINA 427
Db 365 P---DHALIGIVAVVVFVTLCSIFLGRYLASHKGYLTNEAKGADADPADATATINA 420
Qy 428 EGGQNNSEKKEYFI 442
Db 421 EGSQVNAEKEKEYFI 435
```

Search completed: July 7, 2004, 06:02:44
Job time: 64.8289 secs

PS Claim 1; Page 81-82; 97bp; English.

XX The present sequence is a novel human cell surface receptor protein
CC (HCSR) designated HCSR-8. The nucleotide sequence was identified in
CC Inverte Clone 312256 from the CDNA library LUNGNOR02, which was made from
CC RNA isolated from lung tissue. A number of Inverte Clones were used to
CC assemble the consensus sequence. BLAST analysis showed that the sequence
CC is homologous to immuno-superfamily protein 512 g3779242. HCSR and its
CC antagonist are useful for preventing or treating disorders associated
CC with decreased or increased expression or activity of HCSR. Such
CC disorders include cancers such as leukaemia and melanoma, immune
CC disorders such as rheumatoid arthritis, asthma and atherosclerosis,
CC bacterial and parasitic infections and neuronal disorders such as
CC akathisia, Alzheimer's disease, multiple sclerosis and epilepsy.
CC Polynucleotides encoding HCSR may be used as hybridisation probes to
CC diagnose these conditions. Anti-HCSR antibodies may be used as
CC antagonists, as a targeting or delivery mechanism for bringing
CC pharmaceutical agents into contact with cells or tissues expressing HCSR
CC and for diagnosis of HCSR-related disorders. HCSR and its catalytic or
CC immunogenic fragments are useful for drug screening using libraries of
CC compounds

XX Sequence 442 AA;

Query Match 100.0%; Score 2283; DB 3; Length 442;
Best Local Similarity 100.0%; Pred. No. 5.8e-158; Indels 0; Gaps 0;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVTLPSGSCCAAAAAAAPPGLRLRLLLLSAALLPTGDCQNFPTDVTVEGEVA 60
DB 1 MASVTLPSGSCCAAAAAAAPPGLRLRLLLLSAALLPTGDCQNFPTDVTVEGEVA 60
QY 61 TISQVNRKSDSVQLNPNRQITFRDPRRLKRSRLNFSSEKXVLTVNVSISDEG 120
DB 61 TISQVNRKSDSVQLNPNRQITFRDPRRLKRSRLNFSSEKXVLTVNVSISDEG 120
QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKTAVEGEIEVNCNMAKSPATTIRMF 180
DB 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKTAVEGEIEVNCNMAKSPATTIRMF 180
QY 161 KGNTELGKSEVEEWSMWTYTSQMLKHKEDGCVIVICQVEHPATGNLQRYIEVQ 240
DB 161 KGNTELGKSEVEEWSMWTYTSQMLKHKEDGCVIVICQVEHPATGNLQRYIEVQ 240
QY 181 KGNTELGKSEVEEWSMWTYTSQMLKHKEDGCVIVICQVEHPATGNLQRYIEVQ 240
DB 181 KGNTELGKSEVEEWSMWTYTSQMLKHKEDGCVIVICQVEHPATGNLQRYIEVQ 240
QY 241 YKPVHITQMTYPLQGLTRSGDALTECEAIKGPQVWVTVRVVDEKPHAVISGRPLFI 300
DB 241 YKPVHITQMTYPLQGLTRSGDALTECEAIKGPQVWVTVRVVDEKPHAVISGRPLFI 300
QY 301 NNLMKTNDNGTYRCASNIVGKASDVMLYYDPTTIPPTTTTTTTTTTTTTTTTT 360
DB 301 NNLMKTNDNGTYRCASNIVGKASDVMLYYDPTTIPPTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEEGSIRAVDAVAVGVAVVVFAMLCILITIGYPRHKGTYTTHAKGDADA 420
DB 361 SRAGEEGSIRAVDAVAVGVAVVVFAMLCILITIGYPRHKGTYTTHAKGDADA 420
QY 421 DTALINAGGQNNSEKKEFYI 442
DB 421 DTALINAGGQNNSEKKEFYI 442

RESULT 3

ID AA45092 standard; protein; 442 AA.

XX AA45092;

XX 31-MAY-2000 (first entry)

XX Human lymphoid derived dendritic cell adhesion molecule.

XX Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-1;
KW B7-1; T cell proliferation; natural killer cell; NK; tumor cell;

KW biological activity; quality control reagent; treatment; inflammation;
KW immune system disorder; autoimmune; viral infection; infectious disease;
XX organ transplant rejection; bone marrow; modulator; immune response.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..374

FT Peptide 1..38

FT Protein 39..442

FT Modified-site 67..69

FT Modified-site 101..103

FT Modified-site 113..115

FT Modified-site 165..167

FT Modified-site 304..306

FT Modified-site 308..310

FT Domain 375..395

FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

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FT Domain 396..442

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FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

FT Domain 396..442

XX Sequence 442 AA;

Query Match 100.0%; Score 2283; DB 3; Length 442;

Best Local Similarity 100.0%; Pred. No. 5.8e-158; Indels 0; Gaps 0;

Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PS Claim 7; Page 42-43; 44bp; English.

XX The present amino acid sequence is the human lymphoid derived dendritic
XX cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic
XX cells and displays homology to adhesion molecules, B7-1 and cytoplasmic
XX region of B7-1. Human LDCAM is expressed in breast, retina, foetal
XX liver, spleen and heart, lung, muscle, placenta, thyroid and lung
XX carcinoma. LDCAM polypeptides interacts with T cell surface molecules to
XX alter signalling and inhibits T cell proliferation, bind to themselves
XX and B7-1, an LDCAM binding protein and increases natural killer (NK)
XX cell populations. It may be used to measure the biological activity and
XX as quality control reagents of LDCAM binding proteins. LDCAM may be used
XX for treating disorders associated with malfunctioning of immune system,
XX inflammation, autoimmune disorders, viral infected cells, infectious
XX diseases and for killing tumour cells. They are also useful for
XX prevention or reducing the effect of organ and bone marrow transplant
XX rejection and for modulating T cell immune responses. LDCAM polypeptides
XX may also be used as carriers for delivering agents attached to T cells or
XX cells bearing B7-1

QY 1 MASVLPESGSCAAAAAAPPGLRLRLLLLSAALLPTGQONLFTKDVYVIEGEVA 60
 DB 1 MASVLPESGSCAAAAAAPPGLRLRLLLLSAALLPTGQONLFTKDVYVIEGEVA 60
 QY 61 TISQCVKSDSVIQLNPNRQTIYFRDPRPLKDSRFQNLNFSSEELKSLTNVSIISDEG 120
 DB 61 TISQCVKSDSVIQLNPNRQTIYFRDPRPLKDSRFQNLNFSSEELKSLTNVSIISDEG 120
 QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNTAMASKPATITRMF 180
 DB 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNTAMASKPATITRMF 180
 QY 181 KGNTELKGSSEVEEWSMDYTVTSQMLKVKHEDDGVFVICOVHPAYTGNLQYRYLEVO 240
 DB 181 KGNTELKGSSEVEEWSMDYTVTSQMLKVKHEDDGVFVICOVHPAYTGNLQYRYLEVO 240
 QY 241 YKPVHIOMTYPIQGLTREGDALELTCEAIGKPPQVWVTVWRVDEMPQAVISGNPLFI 300
 DB 241 YKPVHIOMTYPIQGLTREGDALELTCEAIGKPPQVWVTVWRVDEMPQAVISGNPLFI 300
 QY 301 NNINKTNGTYRCASNIYGAHSDYMLVYVDPPTIIPPTTTTTTTTTTTTTTTTT 360
 DB 301 NNINKTNGTYRCASNIYGAHSDYMLVYVDPPTIIPPTTTTTTTTTTTTTTTTT 360
 QY 361 SRAGEGSIKRAVDHAVIGVAVVFPMLCLIIIGRYFARHKGTFTHEAKGADDAADA 420
 DB 361 SRAGEGSIKRAVDHAVIGVAVVFPMLCLIIIGRYFARHKGTFTHEAKGADDAADA 420
 QY 421 DTALINAEQGQNNSEKKEYFI 442
 DB 421 DTALINAEQGQNNSEKKEYFI 442

RESULT 4

AAE19887 standard; protein: 442 AA.

AAE19887;

18-JUN-2002 (first entry)

Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.

Human; hepatocellular carcinoma; tumour suppressor lung cancer 1; TSLC1;
 liver; lung; pancreatic cancer; cell proliferative disorder; cytostatic;
 gene therapy.

Homo sapiens.

MO200214557-A1.

21-FEB-2002.

15-AUG-2001; 2001MO-US025690.

15-AUG-2000; 2000US-0225264P.

(UJOY) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

Reeves RH, Yoshinori M;

WPI; 2002-241913/29.

Detecting cell proliferative disorder associated with tumor suppressor
 lung cancer (TSLC) 1 in subject, comprises contacting proliferating cell
 of subject with reagent detecting TSLC1 and detecting modification in
 TSLC1 level.

Disclosure; Page 49-50; 59pp; English.

The invention relates to a method for detecting cell proliferative
 disorder associated with tumour suppressor lung cancer 1 (TSLC1) in a

CC subject. The method comprising contacting a cell component of a
 CC proliferating cell with a reagent that detects level of the cell
 CC component in the proliferating cell and determining modification in the
 CC level of the cell component in proliferating cell as compared with a
 CC healthy cell, where modification indicates disorder associated with
 CC TSLC1. The method is useful for detecting a cell proliferative disorder
 CC (e.g. liver, lung or pancreatic cancer) associated with tumour suppressor
 CC lung cancer 1 (TSLC1) in a subject. The invention is useful in gene
 CC therapy and for treating a cell proliferative disorder such as lung
 CC cancer (human non-small cell lung cancer), liver cancer (hepatocellular
 CC carcinoma) or pancreatic cancer associated with modification of TSLC1
 CC production, where a reagent which modulates (preferably, increases) TSLC1
 CC level in the cells, is employed. The present sequence is human TSLC1
 CC

Sequence 442 AA:

Query Match 100.0%; Score 2283; DB 5; Length 442;

Best Local Similarity 100.0%; Pred. No. 5, 8e-158; Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPESGSCAAAAAAPPGLRLRLLLLSAALLPTGQONLFTKDVYVIEGEVA 60
 DB 1 MASVLPESGSCAAAAAAPPGLRLRLLLLSAALLPTGQONLFTKDVYVIEGEVA 60
 QY 61 TISQCVKSDSVIQLNPNRQTIYFRDPRPLKDSRFQNLNFSSEELKSLTNVSIISDEG 120
 DB 61 TISQCVKSDSVIQLNPNRQTIYFRDPRPLKDSRFQNLNFSSEELKSLTNVSIISDEG 120
 QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNTAMASKPATITRMF 180
 DB 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNTAMASKPATITRMF 180
 QY 181 KGNTELKGSSEVEEWSMDYTVTSQMLKVKHEDDGVFVICOVHPAYTGNLQYRYLEVO 240
 DB 181 KGNTELKGSSEVEEWSMDYTVTSQMLKVKHEDDGVFVICOVHPAYTGNLQYRYLEVO 240
 QY 241 YKPVHIOMTYPIQGLTREGDALELTCEAIGKPPQVWVTVWRVDEMPQAVISGNPLFI 300
 DB 241 YKPVHIOMTYPIQGLTREGDALELTCEAIGKPPQVWVTVWRVDEMPQAVISGNPLFI 300
 QY 301 NNINKTNGTYRCASNIYGAHSDYMLVYVDPPTIIPPTTTTTTTTTTTTTTTTT 360
 DB 301 NNINKTNGTYRCASNIYGAHSDYMLVYVDPPTIIPPTTTTTTTTTTTTTTTTT 360
 QY 361 SRAGEGSIKRAVDHAVIGVAVVFPMLCLIIIGRYFARHKGTFTHEAKGADDAADA 420
 DB 361 SRAGEGSIKRAVDHAVIGVAVVFPMLCLIIIGRYFARHKGTFTHEAKGADDAADA 420
 QY 421 DTALINAEQGQNNSEKKEYFI 442
 DB 421 DTALINAEQGQNNSEKKEYFI 442

RESULT 5

ABP62825 standard; protein: 442 AA.

ABP62825;

14-OCT-2002 (first entry)

Human polypeptide SEQ ID NO 262.

Human; vulnery; dermatological; neuroprotective; nootropic; cancer;
 antiParkinsonian; immunostimulant; cytostatic; immunosuppressive;
 antiidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
 burn; central nervous system disorder; Alzheimer's disease;
 Parkinson's disease; Huntington's disease; immune disorder;
 autoimmune disorder; multiple sclerosis; diabetes; allergy.

Homo sapiens.

WO200218424-A2.

XX 07-MAR-2002.
 PD 31-AUG-2001; 2001WO-US027093.
 XX 01-SEP-2000; 2000US-00654935.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
 PI Zhao QA, Wang D, Liu C, Drmanac RT, Weinman T;
 XX WPI; 2002-583321/62.
 DR N-PSDB; ABQ93304.
 XX
 PT New polynucleotide and polypeptides, useful for treatment and diagnosis
 PT of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
 PT sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
 PT sclerosis, diabetes and allergies.
 XX
 XX Claim 20; SEQ ID NO 262; 284bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising one of
 CC 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising
 CC administering to a mammalian subject a composition comprising the protein
 CC (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
 CC (I), (II) and (III) are useful for diagnostic evaluation of disorders.
 CC (I) is useful for gene therapy of diseases and (II) can be used for
 CC therapeutic treatment. Diseases that may be treated include wound healing
 CC and tissue repair, burns, central nervous system disorders (e.g.
 CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral
 CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 CC sclerosis, diabetes and allergies. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 - XX
 SO Sequence 442 AA;

Query Match 100.0%; Score 2283; DB 5; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.8e-158;
 Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPBGSOCACAAAAAAPPGRRLRLILLLFSAALLIPFGDQNLFTDYVYIEEVA 60
 DB 1 MASVLPBGSOCACAAAAAAPPGRRLRLILLLFSAALLIPFGDQNLFTDYVYIEEVA 60
 QY TISQVKNKSDSVIQLNPNRQTIYFRDPRFLKDSRFQNLNFSSESEKVSITNVSISDEG 120
 DB TISQVKNKSDSVIQLNPNRQTIYFRDPRFLKDSRFQNLNFSSESEKVSITNVSISDEG 120
 QY 121 RYFQOLYTDPPQESYTTITTVVPPRNLMIDIQXTAVGESEIEVNCNMAKSPATTTT 180
 DB 121 RYFQOLYTDPPQESYTTITTVVPPRNLMIDIQXTAVGESEIEVNCNMAKSPATTTT 180
 QY 121 RYFQOLYTDPPQESYTTITTVVPPRNLMIDIQXTAVGESEIEVNCNMAKSPATTTT 180
 DB 121 RYFQOLYTDPPQESYTTITTVVPPRNLMIDIQXTAVGESEIEVNCNMAKSPATTTT 180
 QY 181 KGNTELKSKSEVEEMSDMYTISQMLKVKHEDGVPICVHEPATVGNLQOTRYLEVQ 240
 DB 181 KGNTELKSKSEVEEMSDMYTISQMLKVKHEDGVPICVHEPATVGNLQOTRYLEVQ 240
 QY 241 YKPOVHIOMTYPLQGLTFREGDALEITCEALGKPOVWMTVWRVDEMPQAHVLSGPNLFI 300
 DB 241 YKPOVHIOMTYPLQGLTFREGDALEITCEALGKPOVWMTVWRVDEMPQAHVLSGPNLFI 300
 QY 301 NNLMKTDNGTYRCEASNIVGKASDVMVYVDPPTTTPPTTTTTTTTTTTTTTTTT 360
 DB 301 NNLMKTDNGTYRCEASNIVGKASDVMVYVDPPTTTPPTTTTTTTTTTTTTTTTT 360
 QY 361 SRAGEEGSIRAVDAHVAIGVAAVVFAMLCIIILGRYFAHKGCTYTHEAKGADDAADA 420
 DB 361 SRAGEEGSIRAVDAHVAIGVAAVVFAMLCIIILGRYFAHKGCTYTHEAKGADDAADA 420
 QY 421 DTATINAEQGQNNSEKKEYFI 442
 DB 421 DTATINAEQGQNNSEKKEYFI 442

DB 421 DTATINAEQGQNNSEKKEYFI 442
 RESULT 6
 ID ADA27144
 ID ADA27144 standard; protein; 442 AA.
 XX
 AC ADA27144;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human novel secreted protein from gene 11 #3.
 XX
 XX Cytostatic; antiinflammatory; immunomodulator; neuroprotective;
 KM hemostatic; gene therapy; cancer; inflammation; immune disorder;
 KM neurological disorder; blood clotting disorder; food additive;
 KM preservative; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN US2003055231-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 29-OCT-2001; 2001US-00984130.
 XX
 XX 28-OCT-1998; 98US-0105971P.
 PR 27-OCT-1999; 99WO-US025031.
 PR 19-APR-2000; 2000US-0198407P.
 PR 30-OCT-2000; 2000US-0243792P.
 PR 18-APR-2001; 2001US-00836353.
 XX
 XX (NIJ/) NI J.
 PA (YOUNG/) YOUNG P E.
 PA (KENN/) KENNY J J.
 PA (OLSE/) OLSEN H S.
 PA (MOOR/) MOORE P A.
 PA (WEIT/) WEI Y.
 PA (GREE/) GREENE J M.
 PA (RUBE/) RUBEN S M.
 PA (LIUD/) LIU D.
 PA (CROC/) CROCKER P R.
 XX
 PI Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
 PI Ruben SM, Liu D, Crocker PR;
 XX
 DR WPI; 2003-567103/53.
 XX
 PT New human secreted nucleic acid molecules and polypeptides, useful for
 PT preventing, treating, or ameliorating a medical condition, such as
 PT cancer, inflammation, immune disorders, neurological and blood clotting
 PT disorders.
 XX
 XX Disclosure; Page 72; 454bp; English.
 XX
 CC The invention relates to an isolated nucleic molecule that is at least
 CC 95% identical to 18 human cDNA sequences representing 12 novel genes
 CC encoding secreted proteins or a polynucleotide fragment of the cDNA.
 CC sequence contained in American Type Culture Collection (ATCC) deposit No.
 CC defined in the specification, its species homologue, a variant or allelic
 CC variant of the polynucleotide having a polynucleotide capable of
 CC hybridizing under conditions the polynucleotide, where the polynucleotide
 CC does not hybridize under stringent conditions to a nucleic acid molecule
 CC having a nucleotide sequence of only A or T residues. Also included are
 CC recombinant vectors, host cells (for producing the polypeptide) the
 CC secreted polypeptide (comprising a sequence that is at least 95%
 CC identical to a polypeptide fragment, domain, epitope, full-length
 CC protein, variant, allelic variant or species homologue), antibodies that
 CC specifically bind to the polypeptides, diagnosing, treating, preventing
 CC or ameliorating a medical condition by administering the polynucleotide
 CC or the polypeptide, the gene corresponding to the cDNA sequence and
 CC identifying an activity in a biological assay (by expressing the cDNA
 CC sequence in a cell, isolating the supernatant, and detecting an activity

CC in a biological assay and identifying the protein in the supernatant
 CC having the activity. The polypeptides, nucleic acids and antibodies are
 CC useful for diagnosing a pathological condition or a susceptibility to a
 CC pathological condition, for preventing, treating, or ameliorating a
 CC medical condition, such as cancer, inflammation and other immune
 CC disorders, neuroblastoma and blood clotting disorders (many examples are
 CC given in the specification). The nucleic acids are also useful for
 CC chromosome identification, radiation hybrid mapping or long-range
 CC restriction mapping. The polypeptides and antibodies are useful for
 CC providing immunological probes for differential identification of the
 CC tissues immunohistochemistry assays. The polypeptide, polynucleotide,
 CC agonist or antagonist may also be used as a food additive or preservative
 CC to increase or decrease storage capabilities, fat content or other
 CC nutritional components. The present is a secreted protein of the
 CC invention.

CC Sequence 442 AA;

Query Match 100.0%; Score 2283; DB 6; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.8e-158;
 Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVVLPSGSGCAAAAAAAPPGLRLRLILLLFSAALIPFGDQNLFTKDVTVIEGEVA 60
 DB 1 MASVVLPSGSGCAAAAAAAPPGLRLRLILLLFSAALIPFGDQNLFTKDVTVIEGEVA 60
 QY 61 TISCVNKSDDSVIQLNPNKQTIYFRDFRPLKDSRFQNLNFSSELKVSITNVSISDEG 120
 DB 61 TISCVNKSDDSVIQLNPNKQTIYFRDFRPLKDSRFQNLNFSSELKVSITNVSISDEG 120
 QY 121 RYFCQLYTDPPOESYTTITTVLPPRNLMIDIQKDTAVEGEIEVNCNTAMSKPATITRMF 180
 DB 121 RYFCQLYTDPPOESYTTITTVLPPRNLMIDIQKDTAVEGEIEVNCNTAMSKPATITRMF 180
 QY 121 RYFCQLYTDPPOESYTTITTVLPPRNLMIDIQKDTAVEGEIEVNCNTAMSKPATITRMF 180
 DB 121 RYFCQLYTDPPOESYTTITTVLPPRNLMIDIQKDTAVEGEIEVNCNTAMSKPATITRMF 180
 QY 181 KGNTELKSGSEVEEMSDMTVTTSQMLKVHKEDDGVPIQVHPAVTGNLQOTRYLEVQ 240
 DB 181 KGNTELKSGSEVEEMSDMTVTTSQMLKVHKEDDGVPIQVHPAVTGNLQOTRYLEVQ 240
 QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVAVTWVRVDEMPQHAVISGNLFI 300
 DB 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVAVTWVRVDEMPQHAVISGNLFI 300
 QY 301 NNKKTNDGTYRCASNIIVGKASDMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTT 360
 DB 301 NNKKTNDGTYRCASNIIVGKASDMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTT 360
 QY 361 SRAGEEGSIRAVDAVIGVAVVVFAMLCILILIGRYFARHKGTFTHEAKGADPADDA 420
 DB 361 SRAGEEGSIRAVDAVIGVAVVVFAMLCILILIGRYFARHKGTFTHEAKGADPADDA 420
 QY 421 DTATINAEQGQNNSEKKEVFI 442
 DB 421 DTATINAEQGQNNSEKKEVFI 442

RESULT 7
 ADE54238
 ID ADE54238 standard; protein; 442 AA.

XX ADE54238;
 XX 29-JAN-2004 (first entry)
 XX Human Protein NP_055146, SEQ ID NO 41.
 XX Human; pain; neuronal tissue; gene therapy;
 XX spinal segmental nerve injury; chronic constriction injury; CCI;
 XX spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 XX WO2003016475-A2.
 XX

PD 27-FEB-2003.
 PF 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 XX 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-0333347P.
 XX (GEMO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 PI Woolf C, D'urso D, Befort K, Costigan M,
 XX WPI/ 2003-268312/26.
 XX GENBANK; NP_055148.
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which differentially
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 442 AA;

Query Match 100.0%; Score 2283; DB 7; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.8e-158;
 Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVVLPSGSGCAAAAAAAPPGLRLRLILLLFSAALIPFGDQNLFTKDVTVIEGEVA 60
 DB 1 MASVVLPSGSGCAAAAAAAPPGLRLRLILLLFSAALIPFGDQNLFTKDVTVIEGEVA 60
 QY 61 TISCVNKSDDSVIQLNPNKQTIYFRDFRPLKDSRFQNLNFSSELKVSITNVSISDEG 120
 DB 61 TISCVNKSDDSVIQLNPNKQTIYFRDFRPLKDSRFQNLNFSSELKVSITNVSISDEG 120
 QY 121 RYFCQLYTDPPOESYTTITTVLPPRNLMIDIQKDTAVEGEIEVNCNTAMSKPATITRMF 180
 DB 121 RYFCQLYTDPPOESYTTITTVLPPRNLMIDIQKDTAVEGEIEVNCNTAMSKPATITRMF 180
 QY 181 KGNTELKSGSEVEEMSDMTVTTSQMLKVHKEDDGVPIQVHPAVTGNLQOTRYLEVQ 240
 DB 181 KGNTELKSGSEVEEMSDMTVTTSQMLKVHKEDDGVPIQVHPAVTGNLQOTRYLEVQ 240
 QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVAVTWVRVDEMPQHAVISGNLFI 300
 DB 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVAVTWVRVDEMPQHAVISGNLFI 300

DB 241 YKPOVHIQMTYPLQGLTRGDALELTCEAIKGPQPMVMTWVVDDEMPQHAVLSGPNLFI 300

QY 301 NNUNKTNDGTYRCEASNIYGAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360

DB 301 NNUNKTNDGTYRCEASNIYGAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360

QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILLIGRYFARHKGTYFTHKAGADDAADA 420

DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILLIGRYFARHKGTYFTHKAGADDAADA 420

QY 421 DTALINAEQGQNNSEKKEFYFI 442

DB 421 DTALINAEQGQNNSEKKEFYFI 442

RESULT 8

ADBE6685 standard; protein; 442 AA.

AC ADE86685;

XX 29-JAN-2004 (first entry)

DE Novel human secreted protein #1 associated protein #1.

XX human; secreted protein; cancer; liver disorder; hepatitis;

KM neural disorder; Alzheimer's disease.

XX Homo sapiens.

OS US2003129685-A1.

PN 10-JUL-2003.

PD 18-APR-2001; 2001US-00836353.

PF 28-OCT-1998; 98US-0105971P.

PR 27-OCT-1999; 99WO-US025031.

PR 19-APR-2000; 2000US-0198407P.

XX (N1J1/) NI J.

PA (YOUNG/) YOUNG P E.

PA (KENNY/) KENNY J J.

PA (OLSEN/) OLSEN H S.

PA (MOORE/) MOORE P A.

PA (WEIY/) WEI Y.

PA (GREENE/) GREENE J M.

PA (RUBEN/) RUBEN S M.

PI NI J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;

PI Ruben SM;

XX WPI; 2004-020335/02.

XX New nucleic acid molecule, useful for preparing a medicament for

PT preventing, treating or ameliorating a medical condition e.g. cancer,

PT liver disorders or neural disorders.

XX Disclosure; SEQ ID NO 136; 380pp; English.

XX The invention relates to an isolated nucleic acid sequence, or its

CC allelic variant, a fragment of the cDNA sequence, or its fragment,

CC domain, epitope or species homologue. The nucleic acid is useful for

CC preparing a medicament for preventing, treating or ameliorating a medical

CC condition e.g., cancer, liver disorders such as hepatitis or neural

CC disorders such as Alzheimer's disease. The present sequence represents

CC the amino acid sequence of a novel human secreted protein associated

CC protein.

XX Sequence 442 AA;

Query Match 100.0%; Score 2283; DB 8; Length 442;

Best Local Similarity 100.0%; Pred. No. 5.8e-158;

Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVTLPSGSGQCAAAAAAAPPGLRRLRLLLIFSAALIPEDGQNLFTKDYVTIIEGVA 60

DB 1 MASVTLPSGSGQCAAAAAAAPPGLRRLRLLLIFSAALIPEDGQNLFTKDYVTIIEGVA 60

QY 61 TISQVNRKSDDSVITQLNPNRQTIYRDPKDSRFQNLNSSFELKSLTNVSIISDEG 120

DB 61 TISQVNRKSDDSVITQLNPNRQTIYRDPKDSRFQNLNSSFELKSLTNVSIISDEG 120

QY 121 RYFCQLYTDPPQESYTTITVLVPPNLMIDIKDTAVEGEIEIVNCTAMASKPATIRWF 180

DB 121 RYFCQLYTDPPQESYTTITVLVPPNLMIDIKDTAVEGEIEIVNCTAMASKPATIRWF 180

QY 181 KGNTEKGRSEVEEMSDMTVTLSQMLKVKHEDDGPVLCQVEHPAVGNLTQRYLEVO 240

DB 181 KGNTEKGRSEVEEMSDMTVTLSQMLKVKHEDDGPVLCQVEHPAVGNLTQRYLEVO 240

QY 241 YKPOVHIQMTYPLQGLTRGDALELTCEAIKGPQPMVMTWVVDDEMPQHAVLSGPNLFI 300

DB 241 YKPOVHIQMTYPLQGLTRGDALELTCEAIKGPQPMVMTWVVDDEMPQHAVLSGPNLFI 300

QY 301 NNUNKTNDGTYRCEASNIYGAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360

DB 301 NNUNKTNDGTYRCEASNIYGAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360

QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILLIGRYFARHKGTYFTHKAGADDAADA 420

DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILLIGRYFARHKGTYFTHKAGADDAADA 420

QY 421 DTALINAEQGQNNSEKKEFYFI 442

DB 421 DTALINAEQGQNNSEKKEFYFI 442

RESULT 9

ABO07196 standard; protein; 442 AA.

AC ABO07196;

XX 13-AUG-2003 (first entry)

DE Human p53 modifying protein, SEQ ID 156.

XX Human; p53 modifier; cytosolic; cancer; cytosolic; antiangiogenic;

KM antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;

KM lung cancer; ovarian cancer; angiogenesis; cell cycle;

KM apoptotic disorder; cell proliferation disorder.

XX Homo sapiens.

OS WO20020299122-A1.

PN 12-DEC-2002.

PD 03-JUN-2002; 2002WO-US017382.

PF 05-JUN-2001; 2001US-0296076P.

PR 10-OCT-2001; 2001US-0328605P.

PR 15-FEB-2002; 2002US-0357253P.

XX (EXEL-) EXELIXIS INC.

PI Friedman L, Plozman GD, Belvin M, Francis-Lang H, Li D, Funke RP;

PI WPI; 2003-156859/15.

DR N-PSDB; ACD13371.

XX Identifying modulators of the p53 pathway for use in treating apoptotic

PT or cell proliferation disorders, comprises screening for agents that

PT modulate activity of a human ortholog of genes that modify the p53

PT pathway in Drosophila.

XX Example 2; Page 469-470; 678bp; English.

CC The invention relates to identifying (M1) a candidate p53 pathway
CC modulating agent, by contacting an assay system comprising a purified HM
CC polypeptide (human orthologue of genes that modify the p53 pathway in
CC Drosophila) or nucleic acid with a test agent under conditions, where but
CC for the presence of the test agent, the system provides a reference
CC activity, and detecting a test agent-biased activity of the assay system.
CC Also included are modulating (M2) a p53 pathway of a cell (comprising
CC contacting a cell defective in p53 function with a candidate modulator
CC that specifically binds to a HM polypeptide comprising an HM amino acid
CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
CC in a mammalian cell (comprising contacting the cell with an agent that
CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
CC a disease in a patient (comprising: (a) obtaining a biological sample
CC from the patient; (b) contacting the sample with a probe for HM
CC expression; (c) comparing the results with a control; and (d) determining
CC whether the comparison indicates a likelihood disease). (M1) is useful
CC for identifying modulators of the p53 pathway. A probe for HM expression
CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
CC in a patient, where the cancer has greater than 25 % expression level.
CC Modulators identified by (M1) are useful in a variety of diagnostic and
CC therapeutic applications, where disease or disorder prognosis is related
CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
CC the p53 function of the cell, so that the cell undergoes normal
CC proliferation or progression through the cell cycle. (M2) and (M3) are
CC also useful for treating defects in the p53 pathway such as angiogenic,
CC apoptotic or cell proliferation disorders. The present sequence
CC represents a human p53 pathway modifying protein

XX Sequence 442 AA;

Query Match 99.9%; Score 2280; DB 6; Length 442;

Best Local Similarity 99.8%; Pred. No. 9.6e-158; Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVVLPSGSCAAAAAAPPGLRLRLLLLSAALLPTGQGNLFTKQVTVIGEEVA 60
DB 1 MASVVLPSGSCAAAAAAPPGLRLRLLLLSAALLPTGQGNLFTKQVTVIGEEVA 60
QY 61 TISQVWKSDDSVOLNPNRQTYPRDPRLKDSRQOLNFSSELKXSLTNVSTSDSG 120
DB 61 TISQVWKSDDSVOLNPNRQTYPRDPRLKDSRQOLNFSSELKXSLTNVSTSDSG 120
QY 121 RYFQGLYTPDPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCATNASKPATIRMF 180
DB 121 RYFQGLYTPDPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCATNASKPATIRMF 180
QY 181 KGNTELKSKSEVEMSDMYTTSQMLKVKHEDGVICQVEHPATNGLQRYLVEVQ 240
DB 181 KGNTELKSKSEVEMSDMYTTSQMLKVKHEDGVICQVEHPATNGLQRYLVEVQ 240
QY 181 KGNTELKSKSEVEMSDMYTTSQMLKVKHEDGVICQVEHPATNGLQRYLVEVQ 240
DB 181 KGNTELKSKSEVEMSDMYTTSQMLKVKHEDGVICQVEHPATNGLQRYLVEVQ 240
QY 241 YKPCVHIQMTYPLQGLTREGDALTLTCEAIKGPQVWTVWVDEVPQAVLSGPTLFI 300
DB 241 YKPCVHIQMTYPLQGLTREGDALTLTCEAIKGPQVWTVWVDEVPQAVLSGPTLFI 300
QY 301 NNKLKTDNGYTRCAASNIVGKASHDYLWYVDPPTTIPPTTTTTTTTTTTTTLITD 360
DB 301 NNKLKTDNGYTRCAASNIVGKASHDYLWYVDPPTTIPPTTTTTTTTTTTTTLITD 360
QY 361 SRAGEGSIKAVDAVIGVAVVFMALCLLILIGRYFARHKQTYFTHEAKGADPADADA 420
DB 361 SRAGEGSIKAVDAVIGVAVVFMALCLLILIGRYFARHKQTYFTHEAKGADPADADA 420
QY 421 DTATINAEQGNNSSEKKEFYI 442
DB 421 DTATINAEQGNNSSEKKEFYI 442

RESULT 10

AB007231
ID AB007231 standard; protein; 442 AA.

AC AB007231;

DT 13-AUG-2003 (first entry)

DE Human p53 modifying protein, SEQ ID 191.

KM Human; p53 modifier; cytosolic; cancer; cytostatic; antiangiogenic;
KM antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
KM lung cancer; ovarian cancer; angiogenesis; cell cycle;
KM apoptotic disorder; cell proliferation disorder.

OS Homo sapiens.

PN WO200299122-A1.

PD 12-DEC-2002.

PF 03-JUN-2002; 2002WO-US017382.

PR 05-JUN-2001; 2001US-0296076P.

PR 10-OCT-2001; 2001US-0328605P.

PR 15-FEB-2002; 2002US-0357253P.

PA (EXEL-) EXELIXIS INC.

PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
WPI: 2003-156859/15.

DR N-PSDB; ACD13404.

PT Identifying modulators of the p53 pathway for use in treating apoptotic
PT or cell proliferation disorders, comprises screening for agents that
PT modulate activity of a human ortholog of genes that modify the p53
PT pathway in Drosophila.

PS Example 2; Page 557-559; 678bp; English.

XX The invention relates to identifying (M1) a candidate p53 pathway
CC modulating agent, by contacting an assay system comprising a purified HM
CC polypeptide (human orthologue of genes that modify the p53 pathway in
CC Drosophila) or nucleic acid with a test agent under conditions, where but
CC for the presence of the test agent, the system provides a reference
CC activity, and detecting a test agent-biased activity of the assay system.
CC Also included are modulating (M2) a p53 pathway of a cell (comprising
CC contacting a cell defective in p53 function with a candidate modulator
CC that specifically binds to a HM polypeptide comprising an HM amino acid
CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
CC in a mammalian cell (comprising contacting the cell with an agent that
CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
CC a disease in a patient (comprising: (a) obtaining a biological sample
CC from the patient; (b) contacting the sample with a probe for HM
CC expression; (c) comparing the results with a control; and (d) determining
CC whether the comparison indicates a likelihood disease). (M1) is useful
CC for identifying modulators of the p53 pathway. A probe for HM expression
CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
CC in a patient, where the cancer has greater than 25 % expression level.
CC Modulators identified by (M1) are useful in a variety of diagnostic and
CC therapeutic applications, where disease or disorder prognosis is related
CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
CC the p53 function of the cell, so that the cell undergoes normal
CC proliferation or progression through the cell cycle. (M2) and (M3) are
CC also useful for treating defects in the p53 pathway such as angiogenic,
CC apoptotic or cell proliferation disorders. The present sequence
CC represents a human p53 pathway modifying protein

SQ Sequence 442 AA;

Query Match 99.9%; Score 2280; DB 6; Length 442;

Best Local Similarity 99.8%; Pred. No. 9,6e-158;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPDQGNLFKDVTVIEGEVA 60
DB 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPDQGNLFKDVTVIEGEVA 60
QY 61 TISQVKNKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQLNFSSELKSLTNVISIDEG 120
DB 61 TISQVKNKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQLNFSSELKSLTNVISIDEG 120
QY 121 RYFCQLYTDPPQESYTTITVAVPPRNLMIDIQKOTAVGESEIEVNCTAMASKPATITRMF 180
DB 121 RYFCQLYTDPPQESYTTITVAVPPRNLMIDIQKOTAVGESEIEVNCTAMASKPATITRMF 180
QY 181 KGNTELKGSSEVEEMSDMYTTSQMLKVKHEDDGVPIQVYHAPVATGNLQTORYLEVQ 240
DB 181 KGNTELKGSSEVEEMSDMYTTSQMLKVKHEDDGVPIQVYHAPVATGNLQTORYLEVQ 240
QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVMTVWVVDDEMPQHAVLSGPNLFI 300
DB 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVMTVWVVDDEMPQHAVLSGPNLFI 300
QY 301 NNLNKTDNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
DB 301 NNLNKTDNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTYFTHEAKGADDAADA 420
DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTYFTHEAKGADDAADA 420
QY 421 DTATINABGGQNNSEKKEYFI 442
DB 421 DTATINABGGQNNSEKKEYFI 442

RESULT 11
ADE61605
ID ADE61605 standard; protein; 442 AA.
XX
AC ADE61605;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein AAF69029, SEQ ID NO 7525.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SN1; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; AAF69029.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX

```

PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SN1)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 442 AA;

Query Match 99.9%; Score 2280; DB 7; Length 442;
Best Local Similarity 99.8%; Pred. No. 9,6e-158;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPDQGNLFKDVTVIEGEVA 60
DB 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPDQGNLFKDVTVIEGEVA 60
QY 61 TISQVKNKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQLNFSSELKSLTNVISIDEG 120
DB 61 TISQVKNKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQLNFSSELKSLTNVISIDEG 120
QY 121 RYFCQLYTDPPQESYTTITVAVPPRNLMIDIQKOTAVGESEIEVNCTAMASKPATITRMF 180
DB 121 RYFCQLYTDPPQESYTTITVAVPPRNLMIDIQKOTAVGESEIEVNCTAMASKPATITRMF 180
QY 181 KGNTELKGSSEVEEMSDMYTTSQMLKVKHEDDGVPIQVYHAPVATGNLQTORYLEVQ 240
DB 181 KGNTELKGSSEVEEMSDMYTTSQMLKVKHEDDGVPIQVYHAPVATGNLQTORYLEVQ 240
QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVMTVWVVDDEMPQHAVLSGPNLFI 300
DB 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVMTVWVVDDEMPQHAVLSGPNLFI 300
QY 301 NNLNKTDNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
DB 301 NNLNKTDNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTYFTHEAKGADDAADA 420
DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTYFTHEAKGADDAADA 420
QY 421 DTATINABGGQNNSEKKEYFI 442
DB 421 DTATINABGGQNNSEKKEYFI 442

RESULT 12
ADE61608
ID ADE61608 standard; protein; 442 AA.
XX

```

AC ADE61608;
 XX 29-JAN-2004 (first entry)
 DT
 XX Human Protein AAF69029, SEQ ID NO 7528.
 DE
 XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KM spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 OS
 XX WC2003016475-A2.
 FN
 XX 27-FEB-2003.
 PD
 XX 14-AUG-2002; 2002WO-US025765.
 PF
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 PI MPI; 2003-268312/26.
 DR GENBANK; AAF69029.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017P; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of a polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPD at
 CC ftp.wipo.int/pub/published_pcr_sequences.
 CC
 XX Sequence 442 AA;
 SQ

Query Match 99.9%; Score 2280; DB 7; Length 442;
 Best Local Similarity 99.8%; Pred. No. 9.6e-158;
 Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVTLPSGSCCAAAAAAPPGRLRLILLLFSAALITPGGQNLFTKDVIVIGSEVA 60
 DB 1 MASVTLPSGSCCAAAAAAPPGRLRLILLLFSAALITPGGQNLFTKDVIVIGSEVA 60

QY 61 TISGVNKSDDSVIQLNPNRQTIYFPRDFRLKDSRFQNLNFSSELKVSITNVSISDEG 120
 DB 61 TISGVNKSDDSVIQLNPNRQTIYFPRDFRLKDSRFQNLNFSSELKVSITNVSISDEG 120
 QY 121 RYFCOLYDPPQESYTTITVLVPPRNIMIDIQKDTAVEGEEIEVNCIAMSKEPATIRWF 180
 DB 121 RYFCOLYDPPQESYTTITVLVPPRNIMIDIQKDTAVEGEEIEVNCIAMSKEPATIRWF 180
 QY 181 KGNTELRKSEVEESDMVYVTSQMLKVHEDDGVVTCOVERPATVGNLQTORILEVQ 240
 DB 181 KGNTELRKSEVEESDMVYVTSQMLKVHEDDGVVTCOVERPATVGNLQTORILEVQ 240
 QY 241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPPVMTWVAVDDEMPQAVISGPNLFI 300
 DB 241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPPVMTWVAVDDEMPQAVISGPNLFI 300
 QY 301 NNKNTDNGTYRCEASNIVGRHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTT 360
 DB 301 NNKNTDNGTYRCEASNIVGRHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTT 360
 QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCLLILGRYFARKGTFTHEAKGADADADA 420
 DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCLLILGRYFARKGTFTHEAKGADADADA 420
 QY 421 DTALINAGGQNNSEKKEKYEPI 442
 DB 421 DTALINAGGQNNSEKKEKYEPI 442
 RESULT 13
 AA17830
 ID AA17830 standard; protein; 440 AA.
 AC AA17830;
 XX
 DT 12-AUG-1999 (first entry)
 XX
 DE Human PRO355 protein sequence.
 KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
 KW secreted protein; transmembrane protein; inflammation disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO9928462-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025108.
 XX
 PR 03-DEC-1997; 97US-0067411P. PRO 243
 PR 11-DEC-1997; 97US-0068278P. PRO 241
 PR 11-DEC-1997; 97US-0068338P. PRO 249
 PR 11-DEC-1997; 97US-0069335P. PRO 242
 PR 12-DEC-1997; 97US-0069425P. PRO 244
 PR 16-DEC-1997; 97US-0069694P. PRO 245
 PR 16-DEC-1997; 97US-0069696P. PRO 247
 PR 16-DEC-1997; 97US-0069702P. PRO 248
 PR 17-DEC-1997; 97US-0069870P. PRO 249
 PR 17-DEC-1997; 97US-0068872P. PRO 250
 PR 18-DEC-1997; 97US-0068017P. PRO 251
 PR 05-JAN-1998; 98US-0070440P. PRO 252
 PR 09-FEB-1998; 98US-0074086P. PRO 253
 PR 09-FEB-1998; 98US-0074092P. PRO 254
 PR 25-FEB-1998; 98US-0075945P. PRO 255
 XX
 PA (GENO) GENENTECH INC.
 PI Wood WI, Goddard A, Gurney AL, Yuan J, Baker KP, Chen J;
 XX MPI; 1999-37118/31.
 DR N-PSDB; AAX80055.
 XX

FT Nucleic acids encoding PRO secreted and transmembrane proteins.

XX Claim 12; Fig 27; 123pp; English.

CC The present invention describes nucleic acids encoding PRO secreted and
 CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cytosolic, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy
 CC identification of homologues, raising antibodies and design of probes and
 CC primers. They can be used in a range of diseases related to proteins that
 CC they have homology with, e.g. a PRO protein having homology to complement
 CC proteins may be used in inflammatory responses

XX Sequence 440 AA;

Query Match 99.1%; Score 2263; DB 2; Length 440;
 Best Local Similarity 99.5%; Fred. No. 1.7e-156;
 Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MASVLPESGSCAAAAAAPPGLRLRLLLFSAALIPFGDQNLFTKDVYIEGEVA 60
 DB 1 MASVLPESGSCAAAAAAPPGL--LRLLLLFSAALIPFGDQNLFTKDVYIEGEVA 58
 QY 61 TISQVKNKSDSVIQLNPNRQTYFRDPRPLKDSRFOLLNFSSELKVSITNVSISDEG 120
 DB 59 TISQVKNKSDSVIQLNPNRQTYFRDPRPLKDSRFOLLNFSSELKVSITNVSISDEG 118
 QY 121 RYFCOLYDPPROESTTTTTPVPPRNLMIDIOKTAVERGSEIENCTAMASKPATTRWF 180
 DB 119 RYFCOLYDPPROESTTTTTPVPPRNLMIDIOKTAVERGSEIENCTAMASKPATTRWF 178
 QY 181 KGNTELKSKSEVEEMSDVYVTSQMLKVKHKEDGVPVTCQEHPAVTGNLQTRYLEVQ 240
 DB 179 KGNTELKSKSEVEEMSDVYVTSQMLKVKHKEDGVPVTCQEHPAVTGNLQTRYLEVQ 238
 QY 241 YKPOVHIOMTYPLQGLTRGDALELTCAIGKPPQVMTWVRVDEMPQAHVLSGPNFT 300
 DB 239 YKPOVHIOMTYPLQGLTRGDALELTCAIGKPPQVMTWVRVDEMPQAHVLSGPNFT 298
 QY 301 NNLNKTDNGTYRCESNIVGKAHSDVYLVDPPTTTPPTTTTTTTTTTTTTTTTTTT 360
 DB 299 NNLNKTDNGTYRCESNIVGKAHSDVYLVDPPTTTPPTTTTTTTTTTTTTTTTTTT 358
 QY 361 SRAGEGSGIRAVDAHVIGVAVVVFAMLCIIILGRFAHKKGTFTTHEKGDADA 420
 DB 359 SRAGEGSGIRAVDAHVIGVAVVVFAMLCIIILGRFAHKKGTFTTHEKGDADA 418
 QY 421 DTAINAEQGQNNSEKKEVFI 442
 DB 419 DTAINAEQGQNNSEKKEVFI 440

RESULT 14
 AAB01321
 ID AAB01321 standard; protein; 440 AA.

XX AAB01321;
 AC
 DT 25-SEP-2000 (first entry)
 XX
 DE Human PRO355 polypeptide.

XX PRO; membrane bound protein; secreted protein; PRO357; PRO377; PRO243;
 XX PRO715; PRO241; PRO323; PRO299; PRO323; PRO344; PRO355; PRO353;
 XX PRO361; PRO365; transmembrane polypeptide; antibody; screening;
 XX detection; inhibition; probe; primer; human.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..36

FT Modified-site 9..15
 FT /label= Signal peptide

FT Modified-site /note= "N-myristoylation site"
 FT 65..69
 FT /note= "N-glycosylation site"
 FT 99..103
 FT Modified-site /note= "N-glycosylation site"
 FT 111..115
 FT Modified-site /note= "N-glycosylation site"
 FT 153..167
 FT Modified-site /note= "N-glycosylation site"
 FT 227..233
 FT Modified-site /note= "N-myristoylation site"
 FT 233..240
 FT Modified-site /note= "Tyrosine kinase phosphorylation site"
 FT 302..306
 FT Modified-site /note= "N-glycosylation site"
 FT 306..310
 FT Modified-site /note= "N-glycosylation site"
 FT 307..313
 FT Modified-site /note= "N-myristoylation site"
 FT 319..328
 FT Modified-site /note= "Tyrosine kinase phosphorylation site"
 FT 355..371
 FT Modified-site /note= "N-myristoylation site"
 FT 372..393
 FT Domain /label= Transmembrane domain
 FT 376..382
 FT Modified-site /note= "N-myristoylation site"
 FT 402..408
 FT Modified-site /note= "N-myristoylation site"
 FT 411..417
 FT Modified-site /note= "N-myristoylation site"
 FT 427..433
 FT Modified-site /note= "N-myristoylation site"
 FT 428..432
 FT Modified-site /note= "N-myristoylation site"
 FT 430..434
 FT Modified-site /note= "N-glycosylation site"
 FT /note= "N-glycosylation site"
 PN MO200032776-A2.
 PD 08-JUN-2000.
 XX
 PF 01-DEC-1999; 99WO-US028301.
 XX
 PR 01-DEC-1998; 98WO-US025108.
 PR 16-DEC-1998; 98US-0112850P.
 PR 22-DEC-1998; 98US-0113296P.
 XX
 PA (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E,
 PI Gerlitsen WE, Goddard A, Godowski PJ, Grimaldi CU, Gueney AL,
 PI Hillan KJ, Kijavlin IU, Napier MA, Roy MA, Tumas D, Wood WI;
 XX
 DR WPI; 2000-412324/35.
 DR N-PSDB; AAA95563.
 XX
 PT New human nucleic acids encoding secreted and transmembrane polypeptides,
 PT designated as PRO polypeptides, useful as pharmaceutical and diagnostic
 PT agents.
 XX
 PS Claim 12; Fig 24; 187pp; English.
 XX
 CC New human nucleic acids encoding secreted and transmembrane polypeptides
 CC which are designated as PRO polypeptides are described. The membrane-bound
 CC proteins have various industrial applications, including as
 CC pharmaceutical and diagnostic agents. The membrane-bound proteins can
 CC also be employed for screening of potential peptide or small molecule
 CC inhibitors of the relevant receptor/ligand interaction. Anti-PRO
 CC antibodies are useful for the affinity purification of PRO from
 CC recombinant cell culture or natural sources
 XX
 SQ Sequence 440 AA;

Query Match 99.1%; Score 2263; DB 3; Length 440;
 Best Local Similarity 99.5%; Pred. No. 1,7e-156;
 Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MASVVLPSGSCCAAAAAAPPGLRLRLLLLFSAALIFPTGQONLFTKDVYIEGEVA 60
 DB 1 MASVVLPSGSCCAAAAAAPPGLRLRLLLLFSAALIFPTGQONLFTKDVYIEGEVA 58
 QY 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPRFKDSRQOLNFSSEELKVSILTNVISIDEG 120
 DB 59 TISCQVNSDSDSVIQLNPNRQTIYFRDPRFKDSRQOLNFSSEELKVSILTNVISIDEG 118
 QY 121 RYFCQLYTDPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCJAMASKPATIRMF 180
 DB 119 RYFCQLYTDPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCJAMASKPATIRMF 178
 QY 181 KGNTELKGRSVEWESDMYTTISQMLKVKHEDDGVVICOVHEPAVTGMLQORILEVQ 240
 DB 179 KGNTELKGRSVEWESDMYTTISQMLKVKHEDDGVVICOVHEPAVTGMLQORILEVQ 238
 QY 241 YKPOVHIQMTYPLGLIREGDALETCBAIGKPPQVAVTVWRVDEMPQAVLSGNPLFI 300
 DB 239 YKPOVHIQMTYPLGLIREGDALETCBAIGKPPQVAVTVWRVDEMPQAVLSGNPLFI 298
 QY 301 NNLNKTDNGTYRCASNVKGAHSDYMLYYDPPTTIPPTTTTTTTTTTTTTTTTT 360
 DB 299 NNLNKTDNGTYRCASNVKGAHSDYMLYYDPPTTIPPTTTTTTTTTTTTTTTTT 358
 QY 361 SRAGEEGSIRAVDAVAGVAVVFMCLILLGRYFPAHKGTYFTHAKGADPAADA 420
 DB 359 SRAGEEGSIRAVDAVAGVAVVFMCLILLGRYFPAHKGTYFTHAKGADPAADA 418
 QY 421 DTATINAEQGQNNSEKEKEYFI 442
 DB 419 DTATINAEQGQNNSEKEKEYFI 440

RESULT 15
 AAU29040
 ID AAU29040 standard; protein; 440 AA.
 AC AAU29040;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DB Human PRO polypeptide sequence #17.
 XX
 KW PRO polypeptide; mammary; tumour; cancer; human; cattle; horse; sheep;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200168848-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006530.
 XX
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000WO-US00702P.
 PR 06-MAR-2000; 2000US-0186968P.
 PR 14-MAR-2000; 2000US-0189320P.
 PR 14-MAR-2000; 2000US-0189328P.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000US-0190828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
 PR 21-MAR-2000; 2000US-0191314P.
 PR 28-MAR-2000; 2000US-0192655P.

PR 29-MAR-2000; 2000US-0193032P.
 PR 29-MAR-2000; 2000US-0193053P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 04-APR-2000; 2000US-0194449P.
 PR 04-APR-2000; 2000US-0194647P.
 PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196820P.
 PR 11-APR-2000; 2000US-0196820P.
 PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 PA (GENTH) GENENTECH INC.
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski FJ, Gurney AU;
 PI Pan U, Smith V, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2001-602746/68.
 DR N-PSDB; AAS45941.
 XX
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX
 PS Claim 11; Fig 34; 774pp; English.
 XX
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX

SO Sequence 440 AA;
 Query Match 99.1%; Score 2263; DB 4; Length 440;
 Best Local Similarity 99.5%; Pred. No. 1,7e-156;
 Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MASVVLPSGSCCAAAAAAPPGLRLRLLLLFSAALIFPTGQONLFTKDVYIEGEVA 60
 DB 1 MASVVLPSGSCCAAAAAAPPGLRLRLLLLFSAALIFPTGQONLFTKDVYIEGEVA 58
 QY 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPRFKDSRQOLNFSSEELKVSILTNVISIDEG 120
 DB 59 TISCQVNSDSDSVIQLNPNRQTIYFRDPRFKDSRQOLNFSSEELKVSILTNVISIDEG 118

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Qy 121 RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCSTANASKPATITRMF 180
    |||||
Db 119 RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCSTANASKPATITRMF 178
    |||||
Qy 181 KGNTELKKSSEVEEMSDMYTTSQMLKVKHKEDDGVVICQVEHPATGNLQTORYLEVQ 240
    |||||
Db 179 KGNTELKKSSEVEEMSDMYTTSQMLKVKHKEDDGVVICQVEHPATGNLQTORYLEVQ 238
    |||||
Qy 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVNVWTVRVVDDEMPOHAVLSGPNLFI 300
    |||||
Db 239 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVNVWTVRVVDDEMPOHAVLSGPNLFI 298
    |||||
Qy 301 NNLNKTNDNGTYRCASNIVGKAHSDYMLYVDPPTTIPPTTTTTTTTTTTTTTTTT 360
    |||||
Db 299 NNLNKTNDNGTYRCASNIVGKAHSDYMLYVDPPTTIPPTTTTTTTTTTTTTTTTT 358
    |||||
Qy 361 SRAGEEGSIRAVDAVIGVAVVVPFAMCLLILGRYFARHKGTFTHEAKGADDAADA 420
    |||||
Db 359 SRAGEEGSIRAVDAVIGVAVVVPFAMCLLILGRYFARHKGTFTHEAKGADDAADA 418
    |||||
Qy 421 DTALINAEAGGQNNSEKKEKFI 442
    |||||
Db 419 DTALINAEAGGQNNSEKKEKFI 440
    |||||
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OM protein - protein search, using sw model1

Run on: July 7, 2004, 06:02:51 ; Search time 633.619 Seconds

(without alignments)
217.146 Million cell updates/sec

Title: US-10-622-237-2

Perfect score: 2283

Sequence: 1 MASVLPSSGSCCAAAAAA.....AIINAEQGNSEKKEYFI 442

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2283	100.0	442	9	US-09-778-187B-2
3	2283	100.0	442	10	US-09-984-130-136
4	2283	100.0	442	10	US-09-836-353A-136
5	2283	100.0	442	12	US-10-363-616-262
6	2283	100.0	442	14	US-10-302-041-20
7	2283	100.0	442	14	US-10-403-107-1
8	2283	100.0	442	15	US-10-015-115-111
9	2280	99.9	442	15	US-10-015-115-110
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11	2263	99.1	440	9	US-09-944-449-61
12	2263	99.1	440	9	US-09-944-457-61
13	2263	99.1	440	9	US-09-944-862-61
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15	2263	99.1	440	9	US-09-945-015-61

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17	2263	99.1	440	9	US-09-944-097-61	Sequence 61, Appl
18	2263	99.1	440	9	US-09-944-432-61	Sequence 61, Appl
19	2263	99.1	440	9	US-09-943-762-61	Sequence 61, Appl
20	2263	99.1	440	9	US-09-944-654-61	Sequence 61, Appl
21	2263	99.1	440	9	US-09-943-851A-61	Sequence 61, Appl
22	2263	99.1	440	9	US-09-944-413-61	Sequence 61, Appl
23	2263	99.1	440	9	US-09-944-403-61	Sequence 61, Appl
24	2263	99.1	440	9	US-09-944-896-61	Sequence 61, Appl
25	2263	99.1	440	9	US-09-944-944-61	Sequence 61, Appl
26	2263	99.1	440	9	US-09-944-929-61	Sequence 61, Appl
27	2263	99.1	440	9	US-09-944-907-61	Sequence 61, Appl
28	2263	99.1	440	10	US-09-944-884-61	Sequence 61, Appl
29	2263	99.1	440	10	US-09-944-882-61	Sequence 61, Appl
30	2263	99.1	440	10	US-09-943-780-61	Sequence 61, Appl
31	2263	99.1	440	11	US-09-945-584-61	Sequence 61, Appl
32	2263	99.1	440	12	US-10-206-915-34	Sequence 34, Appl
33	2263	99.1	440	12	US-10-199-670-34	Sequence 34, Appl
34	2263	99.1	440	12	US-10-201-858-34	Sequence 34, Appl
35	2263	99.1	440	12	US-10-205-890-34	Sequence 34, Appl
36	2263	99.1	440	12	US-10-208-024-34	Sequence 34, Appl
37	2263	99.1	440	12	US-10-201-853-34	Sequence 34, Appl
38	2263	99.1	440	12	US-10-677-471-61	Sequence 61, Appl
39	2263	99.1	440	12	US-10-677-669-61	Sequence 61, Appl
40	2263	99.1	440	12	US-10-174-581-34	Sequence 34, Appl
41	2263	99.1	440	12	US-10-176-749-34	Sequence 34, Appl
42	2263	99.1	440	12	US-10-176-514-34	Sequence 34, Appl
43	2263	99.1	440	12	US-10-176-915-34	Sequence 34, Appl
44	2263	99.1	440	12	US-10-176-464-34	Sequence 34, Appl
45	2263	99.1	440	12	US-10-176-464-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-778-510-20
Sequence 20, Application US/09778510
Patent No. US20020164686A1
GENERAL INFORMATION:
Applicant: Baum, Peter
Title of Invention: Molecules Designated B7L1
File Reference: 2844-US
Current Application Number: US/09/778, 510
Current Filing Date: 2001-02-07
Prior Application Number: PCT/US99/17906
Prior Filing Date: 1999-08-05
Prior Application Number: 60/095, 663
Prior Filing Date: 1998-08-07
Number of Seq ID NOS: 22
Software: PatentIn Ver. 2.0
Seq ID NO 20
Length: 442
Type: PRT
Organism: Homo sapien
US-09-778-510-20

Query Match 100.0%; Score 2283; DB 9; Length 442;
Best Local Similarity 100.0%; Pred. No. 9.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPSSGSCCAAAAAAAPPRLRLRLILFSAALIPFGDGNLFTKDVVIGEVA 60
Db 1 MASVLPSSGSCCAAAAAAAPPRLRLRLILFSAALIPFGDGNLFTKDVVIGEVA 60

QY 61 TISQVKKSDSYIQLNPKRTIYPRDRPLKDSFOLLNBSSELKSLTNVSISSDG 120
Db 61 TISQVKKSDSYIQLNPKRTIYPRDRPLKDSFOLLNBSSELKSLTNVSISSDG 120

QY 121 RYFCQLYTDPQSSYTTITVLPVPPRMIMDIOQDVESEIEVNTAASKPATIRMF 180
Db 121 RYFCQLYTDPQSSYTTITVLPVPPRMIMDIOQDVESEIEVNTAASKPATIRMF 180

QY 181 KGNTELKKGSEVEEMSDMYTAVTSQLMLKVHKEDDGPVYICOVEHPAVTGNLQOTORYLEVO 240
DB 181 KGNTELKKGSEVEEMSDMYTAVTSQLMLKVHKEDDGPVYICOVEHPAVTGNLQOTORYLEVO 240
QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVWVTVWRVVDENPOHAYLSGPNLFI 300
DB 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVWVTVWRVVDENPOHAYLSGPNLFI 300
QY 301 NNUNKTNDGTYRCESASNIIVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360
DB 301 NNUNKTNDGTYRCESASNIIVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKRAVDHAVIGVAVVAVVFAMLCLIIILGRYFAHKGTYFTHEAKGADDAADA 420
DB 361 SRAGEGSIKRAVDHAVIGVAVVAVVFAMLCLIIILGRYFAHKGTYFTHEAKGADDAADA 420
QY 421 DTAIINAEQGNSEKKEEYFI 442
DB 421 DTAIINAEQGNSEKKEEYFI 442

RESULT 2

US-09-778-187B-2
; Sequence 2, Application US/09778187B
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Farnlow III, William C
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187B
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: US 60/095,672
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 442
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-778-187B-2

Query Match 100.0%; Score 2283; DB 9; Length 442;
Best Local Similarity 100.0%; Pred. No. 9.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPFGDQNLFTKDVTVIEGEVA 60
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DB 61 TISQVNSKSDSVIQLNPNKQTIYFRDFRPLKDSRFQOLNFSSELKVSILTVNISIDEG 120
QY 121 RYFCOLYTDPPQESYTTITVLPVRNLMIDIQKDTAVEGSEIEVNCIAMSXPATTTIRMF 180
DB 121 RYFCOLYTDPPQESYTTITVLPVRNLMIDIQKDTAVEGSEIEVNCIAMSXPATTTIRMF 180
QY 181 KGNTELKKGSEVEEMSDMYTAVTSQLMLKVHKEDDGPVYICOVEHPAVTGNLQOTORYLEVO 240
DB 181 KGNTELKKGSEVEEMSDMYTAVTSQLMLKVHKEDDGPVYICOVEHPAVTGNLQOTORYLEVO 240
QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVWVTVWRVVDENPOHAYLSGPNLFI 300
DB 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVWVTVWRVVDENPOHAYLSGPNLFI 300
QY 301 NNUNKTNDGTYRCESASNIIVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360
DB 301 NNUNKTNDGTYRCESASNIIVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKRAVDHAVIGVAVVAVVFAMLCLIIILGRYFAHKGTYFTHEAKGADDAADA 420

DB 361 SRAGEGSIKRAVDHAVIGVAVVAVVFAMLCLIIILGRYFAHKGTYFTHEAKGADDAADA 420
QY 421 DTAIINAEQGNSEKKEEYFI 442
DB 421 DTAIINAEQGNSEKKEEYFI 442

RESULT 3

US-09-984-130-136
; Sequence 136, Application US/09984130
; Publication No. US20030055231A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PFA89P2
; CURRENT APPLICATION NUMBER: US/09/984,130
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-130-136

Query Match 100.0%; Score 2283; DB 10; Length 442;
Best Local Similarity 100.0%; Pred. No. 9.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPFGDQNLFTKDVTVIEGEVA 60
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DB 61 TISQVNSKSDSVIQLNPNKQTIYFRDFRPLKDSRFQOLNFSSELKVSILTVNISIDEG 120
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DB 121 RYFCOLYTDPPQESYTTITVLPVRNLMIDIQKDTAVEGSEIEVNCIAMSXPATTTIRMF 180
QY 181 KGNTELKKGSEVEEMSDMYTAVTSQLMLKVHKEDDGPVYICOVEHPAVTGNLQOTORYLEVO 240
DB 181 KGNTELKKGSEVEEMSDMYTAVTSQLMLKVHKEDDGPVYICOVEHPAVTGNLQOTORYLEVO 240
QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVWVTVWRVVDENPOHAYLSGPNLFI 300
DB 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVWVTVWRVVDENPOHAYLSGPNLFI 300
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QY 361 SRAGEGSIKRAVDHAVIGVAVVAVVFAMLCLIIILGRYFAHKGTYFTHEAKGADDAADA 420
DB 361 SRAGEGSIKRAVDHAVIGVAVVAVVFAMLCLIIILGRYFAHKGTYFTHEAKGADDAADA 420
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DB 421 DTAIINAEQGNSEKKEEYFI 442

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RESULT 4
US-09-836-353A-136
; Sequence 136, Application US/09836353A
; Publication No. US20030129685A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P1
; CURRENT APPLICATION NUMBER: US/09/836,353A
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-353A-136

Query Match          100.0%; Score 2283; DB 10; Length 442;
Best Local Similarity 100.0%; Pred. No. 9,1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPFGDGNLFTKDVTVIEGEVA 60
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Cy 61 TISQVKNKSDSDSVIQLNPNRQTIYFRDPRPKDSRFQLNFSSESEKVLTVNSISDEG 120
Db 61 TISQVKNKSDSDSVIQLNPNRQTIYFRDPRPKDSRFQLNFSSESEKVLTVNSISDEG 120
Cy 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKTAVEGEIEVNCCTAASKPATITRMF 180
Db 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKTAVEGEIEVNCCTAASKPATITRMF 180
Cy 181 KGNTELKSKSEVEEMSDMTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVQ 240
Db 181 KGNTELKSKSEVEEMSDMTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVQ 240
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Db 241 YKPOVHIQMTYPLQGLTREGDALELTCEALIGKPOVMTWVRVDDEMPQHAVALSGPNLFI 300
Cy 301 NNLNKTNDGTYRCEASNIYGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
Db 301 NNLNKTNDGTYRCEASNIYGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
Cy 361 SRAGEEGSIRAVDAVAVIGVAVVVFAMLCIIILIGRYFAHKGTYFTHEAKGADDAADA 420
Db 361 SRAGEEGSIRAVDAVAVIGVAVVVFAMLCIIILIGRYFAHKGTYFTHEAKGADDAADA 420
Cy 421 DTALINAEAGGQNNSEKKEYFI 442
Db 421 DTALINAEAGGQNNSEKKEYFI 442

RESULT 5
US-10-363-616-262
; Sequence 262, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01

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; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 262
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-262

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Best Local Similarity 100.0%; Pred. No. 9,1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKTAVEGEIEVNCCTAASKPATITRMF 180
Db 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKTAVEGEIEVNCCTAASKPATITRMF 180
Cy 181 KGNTELKSKSEVEEMSDMTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVQ 240
Db 181 KGNTELKSKSEVEEMSDMTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVQ 240
Cy 241 YKPOVHIQMTYPLQGLTREGDALELTCEALIGKPOVMTWVRVDDEMPQHAVALSGPNLFI 300
Db 241 YKPOVHIQMTYPLQGLTREGDALELTCEALIGKPOVMTWVRVDDEMPQHAVALSGPNLFI 300
Cy 301 NNLNKTNDGTYRCEASNIYGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
Db 301 NNLNKTNDGTYRCEASNIYGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
Cy 361 SRAGEEGSIRAVDAVAVIGVAVVVFAMLCIIILIGRYFAHKGTYFTHEAKGADDAADA 420
Db 361 SRAGEEGSIRAVDAVAVIGVAVVVFAMLCIIILIGRYFAHKGTYFTHEAKGADDAADA 420
Cy 421 DTALINAEAGGQNNSEKKEYFI 442
Db 421 DTALINAEAGGQNNSEKKEYFI 442

RESULT 6
US-10-302-041-20
; Sequence 20, Application US/10302041
; Publication No. US20030144478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/10/302,041
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-302-041-20

Query Match          100.0%; Score 2283; DB 14; Length 442;
Best Local Similarity 100.0%; Pred. No. 9,1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPFGDGNLFTKDVTVIEGEVA 60

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Db 1 MASVVLPSGSCCAAAAAAARPGRLRLLLLLLFSAALLIFPGDQNLFTKDVIVIEEVA 60
Qy 61 TISQVWKSDDSVQLNPNKQITIFRDFRPLKDSRFQOLNPFSSSELKVSILTIVSISDEG 120
Db 61 TISQVWKSDDSVQLNPNKQITIFRDFRPLKDSRFQOLNPFSSSELKVSILTIVSISDEG 120
Qy 121 RYFQOLYTPDPOESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNMAASKPATITIRMF 180
Db 121 RYFQOLYTPDPOESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNMAASKPATITIRMF 180
Qy 181 KGNTELKGSVEEWSMDYITVTSQMLKVKHKEDDGVVICQVEHPATGNLQORYLEVQ 240
Db 181 KGNTELKGSVEEWSMDYITVTSQMLKVKHKEDDGVVICQVEHPATGNLQORYLEVQ 240
Qy 241 YKPOVHIQMTYPLQGLTREGDALETCBAIGKPOVWVTVWRVDDEMPQAHVLSGNPLFI 300
Db 241 YKPOVHIQMTYPLQGLTREGDALETCBAIGKPOVWVTVWRVDDEMPQAHVLSGNPLFI 300
Qy 301 NNLNKTNDNGTYRCEASNIVGKASDYMLYVDPPTIIPPTTTTTTTTTTTTTTTTT 360
Db 301 NNLNKTNDNGTYRCEASNIVGKASDYMLYVDPPTIIPPTTTTTTTTTTTTTTTTT 360
Qy 361 SRAGEEGSIRAVDAVAVIGVAVVAVFAMLCILILGRYFARHKGTFTHEAKGADDAADA 420
Db 361 SRAGEEGSIRAVDAVAVIGVAVVAVFAMLCILILGRYFARHKGTFTHEAKGADDAADA 420
Qy 421 DTALINAEQGQNNSEKKEYFI 442
Db 421 DTALINAEQGQNNSEKKEYFI 442

RESULT 7

US-10-403-107-1
; Sequence 1, Application US/10403107
; Publication No. US20030165974A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: YOSHINO, Mairamaki
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHU1770-1
; CURRENT APPLICATION NUMBER: US/10/403,107
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/930,803
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-107-1

Query Match 100.0%; Score 2283; DB 14; Length 442;
Best Local Similarity 100.0%; Pred. No. 9,1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASVVLPSGSCCAAAAAAARPGRLRLLLLLLFSAALLIFPGDQNLFTKDVIVIEEVA 60
Db 1 MASVVLPSGSCCAAAAAAARPGRLRLLLLLLFSAALLIFPGDQNLFTKDVIVIEEVA 60
Qy 61 TISQVWKSDDSVQLNPNKQITIFRDFRPLKDSRFQOLNPFSSSELKVSILTIVSISDEG 120
Db 61 TISQVWKSDDSVQLNPNKQITIFRDFRPLKDSRFQOLNPFSSSELKVSILTIVSISDEG 120
Qy 121 RYFQOLYTPDPOESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNMAASKPATITIRMF 180
Db 121 RYFQOLYTPDPOESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNMAASKPATITIRMF 180
Qy 181 KGNTELKGSVEEWSMDYITVTSQMLKVKHKEDDGVVICQVEHPATGNLQORYLEVQ 240
Db 181 KGNTELKGSVEEWSMDYITVTSQMLKVKHKEDDGVVICQVEHPATGNLQORYLEVQ 240

Qy 241 YKPOVHIQMTYPLQGLTREGDALETCBAIGKPOVWVTVWRVDDEMPQAHVLSGNPLFI 300
Db 241 YKPOVHIQMTYPLQGLTREGDALETCBAIGKPOVWVTVWRVDDEMPQAHVLSGNPLFI 300
Qy 301 NNLNKTNDNGTYRCEASNIVGKASDYMLYVDPPTIIPPTTTTTTTTTTTTTTTTT 360
Db 301 NNLNKTNDNGTYRCEASNIVGKASDYMLYVDPPTIIPPTTTTTTTTTTTTTTTTT 360
Qy 361 SRAGEEGSIRAVDAVAVIGVAVVAVFAMLCILILGRYFARHKGTFTHEAKGADDAADA 420
Db 361 SRAGEEGSIRAVDAVAVIGVAVVAVFAMLCILILGRYFARHKGTFTHEAKGADDAADA 420
Qy 421 DTALINAEQGQNNSEKKEYFI 442
Db 421 DTALINAEQGQNNSEKKEYFI 442

RESULT 8

US-10-015-115-111
; Sequence 11, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zethusen, Bryan D
; APPLICANT: Patruzajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangoli, Basha A
; APPLICANT: Shinkels, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-111

Query Match 100.0%; Score 2283; DB 15; Length 442;
Best Local Similarity 100.0%; Pred. No. 9,1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASVVLPSGSCCAAAAAAARPGRLRLLLLLLFSAALLIFPGDQNLFTKDVIVIEEVA 60
Db 1 MASVVLPSGSCCAAAAAAARPGRLRLLLLLLFSAALLIFPGDQNLFTKDVIVIEEVA 60
Qy 61 TISQVWKSDDSVQLNPNKQITIFRDFRPLKDSRFQOLNPFSSSELKVSILTIVSISDEG 120

Db 61 TISCQVNSDDSVIQLNPNKQTYFRDRLKDSRQLNFSSESEKVSLTNVSISDEG 120
Qy 121 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVGEIEIVNCTAMASKPATITRMF 180
Db 121 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVGEIEIVNCTAMASKPATITRMF 180
Qy 181 KGNTELKGSSEVEBMSDMYTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQOTRYLEVO 240
Db 181 KGNTELKGSSEVEBMSDMYTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQOTRYLEVO 240
Qy 241 YKPOVHIQMTYPLQGLTRFGDALBELTCEAIGKPPQVMTWVRVDEMPQHAVISGPNLFI 300
Db 241 YKPOVHIQMTYPLQGLTRFGDALBELTCEAIGKPPQVMTWVRVDEMPQHAVISGPNLFI 300
Qy 301 NNLMKTDNGTYRCESNIVGKAHSDYMLVYDPPPTTIPPTTTTTTTTTTTTTTTTT 360
Db 301 NNLMKTDNGTYRCESNIVGKAHSDYMLVYDPPPTTIPPTTTTTTTTTTTTTTTTT 360
Qy 361 SRAGEGSIKRAVDHAIIGVAVVAVFAMCLIIIGRYFARKGTYFTHKAGADDAADA 420
Db 361 SRAGEGSIKRAVDHAIIGVAVVAVFAMCLIIIGRYFARKGTYFTHKAGADDAADA 420
Qy 421 DTALINAEQGQNNSEKKEYFI 442
Db 421 DTALINAEQGQNNSEKKEYFI 442

RESULT 9

US-10-015-115-110
; Sequence 110, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zernhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangoli, Esna A
; APPLICANT: Shinkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; TYPE: PRT
; LENGTH: 442
; ORGANISM: Homo sapiens
US-10-015-115-110

Query Match 99.9%; Score 2280; DB 15; Length 442;
Best Local Similarity 99.8%; Pred No. 1,6e-176;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASVVLPSGSGQCAAAAAAAPPGLRLRLLLLFSAALIPDGGQNLFTKDYVIEGEVA 60
Db 1 MASVVLPSGSGQCAAAAAAAPPGLRLRLLLLFSAALIPDGGQNLFTKDYVIEGEVA 60
Qy 61 TISCQVNSDDSVIQLNPNKQTYFRDRLKDSRQLNFSSESEKVSLTNVSISDEG 120
Db 61 TISCQVNSDDSVIQLNPNKQTYFRDRLKDSRQLNFSSESEKVSLTNVSISDEG 120
Qy 121 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVGEIEIVNCTAMASKPATITRMF 180
Db 121 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVGEIEIVNCTAMASKPATITRMF 180
Qy 181 KGNTELKGSSEVEBMSDMYTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQOTRYLEVO 240
Db 181 KGNTELKGSSEVEBMSDMYTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQOTRYLEVO 240
Qy 241 YKPOVHIQMTYPLQGLTRFGDALBELTCEAIGKPPQVMTWVRVDEMPQHAVISGPNLFI 300
Db 241 YKPOVHIQMTYPLQGLTRFGDALBELTCEAIGKPPQVMTWVRVDEMPQHAVISGPNLFI 300
Qy 301 NNLMKTDNGTYRCESNIVGKAHSDYMLVYDPPPTTIPPTTTTTTTTTTTTTTTTT 360
Db 301 NNLMKTDNGTYRCESNIVGKAHSDYMLVYDPPPTTIPPTTTTTTTTTTTTTTTTT 360
Qy 361 SRAGEGSIKRAVDHAIIGVAVVAVFAMCLIIIGRYFARKGTYFTHKAGADDAADA 420
Db 361 SRAGEGSIKRAVDHAIIGVAVVAVFAMCLIIIGRYFARKGTYFTHKAGADDAADA 420
Qy 421 DTALINAEQGQNNSEKKEYFI 442
Db 421 DTALINAEQGQNNSEKKEYFI 442

RESULT 10

US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gutrey, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; TYPE: PRT
; LENGTH: 440
; ORGANISM: Homo sapien
US-09-866-028-61

Query Match

99.1%; Score 2263; DB 9; Length 440;

Best Local Similarity 99.5%; Pred: No. 3.8e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1

QY	1	MAVAVLPSSGGCCAAAAAARPGRLRLILLFSAALAIPTDQGNLFTTKQVYIEGVA	60
Db	1	MAVAVLPSSGGCCAAAAAARPG--LRLLLLFSAALAIPTDQGNLFTTKQVYIEGVA	58
QY	61	TISGQVNSKDDSVYQLLNNRQTIYFRDFRLKDSRFOLLNFSSELKVSILTNVISDEG	120
Db	59	TISGQVNSKDDSVYQLLNNRQTIYFRDFRPLKDSRFOLLNFSSELKVSILTNVISDEG	118
QY	121	RYFCQLYTPDPOESYTTITVLVPRRLIMDICKDAVEGEELEVNCSTMAKSPATTRMF	180
Db	119	RYFCQLYTPDPOESYTTITVLVPRRLIMDICKDAVEGEBELVNCSTMAKSPATTRMF	178
QY	181	KGNTELKGSVEEWSMDYTVTSQMLKVKHEDDGPVICOVEHNAVGNLQTORYLEVQ	240
Db	179	KGNTELKGSVEEWSMDYTVTSQMLKVKHEDDGPVICOVEHNAVGNLQTORYLEVQ	238
QY	241	YKQVQVIMTYPLQGLTREGDALELTCEAIGKQVQVMTWRYVDENMGHVAISGPNLFI	300
Db	239	YKQVQVIMTYPLQGLTREGDALELTCEAIGKQVQVMTWRYVDENMGHVAISGPNLFI	298
QY	301	NNLNKTDNGTYRCASNIYGKAHSDYMLVYDPTTIEPPTTTTTTTTTTTTTLLITTD	360
Db	299	NNLNKTDNGTYRCASNIYGKAHSDYMLVYDPTTIEPPTTTTTTTTTTTTTLLITTD	358
QY	361	SRAEGEGSIRAVDHAIVGGVAVVVFAMCLIIIGRYPARHKGTYFTHEAKGADDAADA	420
Db	359	SRAEGEGSIRAVDHAIVGGVAVVVFAMCLIIIGRYFAAHKGTYFTHEAKGADDAADA	418
QY	421	DTAIIAEGGQNNSEKKKEYFI 442	
Db	419	DTAIIAEGGQNNSEKKKEYFI 440	

RESULT 11
US-09-944-449-61

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerlitsen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kljavin, Ivar
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tomas, Daniel
 APPLICANT: Wood, William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P2548P1C1
 CURRENT APPLICATION NUMBER: US/09/944,449
 CURRENT FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 09/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/067,411
 PRIOR FILING DATE: December 3, 1997
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,378
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,425

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1 PRIOR FILLING DATE: December 12, 1997
2 PRIOR APPLICATION NUMBER: 50/069,696
3 PRIOR FILLING DATE: December 15, 1997
4 PRIOR APPLICATION NUMBER: 50/069,694
5 PRIOR FILLING DATE: December 15, 1997
6 PRIOR APPLICATION NUMBER: 50/069,702
7 PRIOR FILLING DATE: December 15, 1997
8 PRIOR APPLICATION NUMBER: 50/069,870
9 PRIOR FILLING DATE: December 17, 1997
10 PRIOR APPLICATION NUMBER: 50/069,873
11 PRIOR FILLING DATE: December 17, 1997
12 PRIOR APPLICATION NUMBER: 50/068,017
13 PRIOR FILLING DATE: December 18, 1997
14 PRIOR APPLICATION NUMBER: 50/070,440
15 PRIOR FILLING DATE: January 5, 1998
16 PRIOR APPLICATION NUMBER: 50/074,086
17 PRIOR FILLING DATE: February 9, 1998
18 PRIOR APPLICATION NUMBER: 50/074,092
19 PRIOR FILLING DATE: February 9, 1998
20 PRIOR APPLICATION NUMBER: 50/075,945
21 PRIOR FILLING DATE: February 25, 1998
22 PRIOR APPLICATION NUMBER: 50/112,850
23 PRIOR FILLING DATE: December 15, 1998
24 PRIOR APPLICATION NUMBER: 50/113,296
25 PRIOR FILLING DATE: December 22, 1998
26 PRIOR APPLICATION NUMBER: 50/146,222
27 PRIOR FILLING DATE: July 28, 1999
28 PRIOR APPLICATION NUMBER: PCT/US99/19330
29 PRIOR FILLING DATE: September 15, 1998
30 PRIOR APPLICATION NUMBER: PCT/US98/5108
31 PRIOR FILLING DATE: December 1, 1998
32 PRIOR APPLICATION NUMBER: 09/216,021
33 PRIOR FILLING DATE: December 15, 1998
34 PRIOR APPLICATION NUMBER: 09/218,517
35 PRIOR FILLING DATE: December 22, 1998
36 PRIOR APPLICATION NUMBER: 09/254,311
37 PRIOR FILLING DATE: March 3, 1999
38 PRIOR APPLICATION NUMBER: PCT/US99/12252
39 PRIOR FILLING DATE: June 22, 1999
40 PRIOR APPLICATION NUMBER: PCT/US99/21090
41 PRIOR FILLING DATE: September 15, 1999
42 PRIOR APPLICATION NUMBER: PCT/US99/28409
43 PRIOR FILLING DATE: No. US20020106474/Alamber 30, 1999
44 PRIOR APPLICATION NUMBER: PCT/US99/28313
45 PRIOR FILLING DATE: No. US20020106474/Alamber 30, 1999
46 PRIOR APPLICATION NUMBER: PCT/US99/28301
47 PRIOR FILLING DATE: December 1, 1999
48 PRIOR APPLICATION NUMBER: PCT/US99/30095
49 PRIOR FILLING DATE: December 15, 1999
50 PRIOR APPLICATION NUMBER: PCT/US00/03565
51 PRIOR FILLING DATE: February 11, 2000
52 PRIOR APPLICATION NUMBER: PCT/US00/04414
53 PRIOR FILLING DATE: February 22, 2000
54 PRIOR APPLICATION NUMBER: PCT/US00/05841
55 PRIOR FILLING DATE: March 2, 2000
56 PRIOR APPLICATION NUMBER: PCT/US00/08439
57 PRIOR FILLING DATE: March 30, 2000
58 PRIOR APPLICATION NUMBER: PCT/US00/14042
59 PRIOR FILLING DATE: May 22, 2000
60 PRIOR APPLICATION NUMBER: PCT/US00/20710
61 PRIOR FILLING DATE: July 28, 2000
62 PRIOR APPLICATION NUMBER: PCT/US00/32678
63 PRIOR FILLING DATE: December 1, 2000
64 PRIOR APPLICATION NUMBER: PCT/US01/06520
65 PRIOR FILLING DATE: February 28, 2001
66 NUMBER OF SEQ ID NOS: 120
67 SEQ ID NO 61
68 LENGTH: 440
69 TYPE: PRT
70 ORGANISM: Homo Sapien
71 US-09-944-4749-61

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Query Match 99.1%; Score 2263; DB 9; Length 440;

Best Local Similarity 99.5%; Pred. No. 3.8e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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QY 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALITGDCQNLFTKDVIVIEGEVA 60
Db 1 MASVLPSSGSCAAAAAAPPGL--LRLLLLLFSAALITGDCQNLFTKDVIVIEGEVA 58
QY 61 TISQVWKKSDSVYQLNPNRQITTFPRDKSRQQLNFSSESKVSLTNVSIISDEG 120
Db 59 TISQVWKKSDSVYQLNPNRQITTFPRDKSRQQLNFSSESKVSLTNVSIISDEG 118
QY 121 RYFQQLTDPPOESYTTITVLPFRNLMIDQKDTAEGEIEIENCTAMASKZATTIRWF 180
Db 119 RYFQQLTDPPOESYTTITVLPFRNLMIDQKDTAEGEIEIENCTAMASKZATTIRWF 178
QY 181 KGNTELKGSKEVEEWSMVTYTSQMLKVKHEDDGVFVICOVEHPAVTGNLQTORYLEVQ 240
Db 179 KGNTELKGSKEVEEWSMVTYTSQMLKVKHEDDGVFVICOVEHPAVTGNLQTORYLEVQ 238
QY 241 YKPVHLOMTYPLQGLTREGDALITCEALGKPOVAVTWVRVDEMPQHAVISGPRLLFI 300
Db 239 YKPVHLOMTYPLQGLTREGDALITCEALGKPOVAVTWVRVDEMPQHAVISGPRLLFI 298
QY 301 NNLNKTNGTYRCASNIVGKAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTLITD 360
Db 299 NNLNKTNGTYRCASNIVGKAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTLITD 358
QY 361 SRAGEBSIRAVDAVAVGVAVVFMCLLILGSPFAHKTCTYTHAKGADPDADA 420
Db 359 SRAGEBSIRAVDAVAVGVAVVFMCLLILGSPFAHKTCTYTHAKGADPDADA 418
QY 421 DTALINAGGQNNSEKKEFYI 442
Db 419 DTALINAGGQNNSEKKEFYI 440
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RESULT 12

US-09-944-457-61
Sequence 61, Application US/09944457
Patent No. US20020110859A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Bocstein, David

APPLICANT: Baton, Dan

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

APPLICANT: Gutney, Austin

APPLICANT: Hillan, Kenneth

APPLICANT: Kijavini, Ivar

APPLICANT: Napier, Mary

APPLICANT: Roy, Margaret

APPLICANT: Tumas, Daniel

APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P2548P1C1

CURRENT APPLICATION NUMBER: US/09/944.457

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 09/866,028

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR FILING DATE: December 3, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,335

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,425

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,425

PRIOR FILING DATE: December 12, 1997

PRIOR APPLICATION NUMBER: 60/069,696

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,694

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,702

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,870

PRIOR FILING DATE: December 17, 1997

PRIOR APPLICATION NUMBER: 60/069,873

PRIOR FILING DATE: December 17, 1997

PRIOR APPLICATION NUMBER: 60/068,017

PRIOR FILING DATE: December 18, 1997

PRIOR APPLICATION NUMBER: 60/070,440

PRIOR FILING DATE: January 5, 1998

PRIOR APPLICATION NUMBER: 60/074,086

PRIOR FILING DATE: February 9, 1998

PRIOR APPLICATION NUMBER: 60/074,092

PRIOR FILING DATE: February 9, 1998

PRIOR APPLICATION NUMBER: 60/075,945

PRIOR FILING DATE: February 25, 1998

PRIOR APPLICATION NUMBER: 60/112,850

PRIOR FILING DATE: December 16, 1998

PRIOR APPLICATION NUMBER: 60/113,296

PRIOR FILING DATE: December 22, 1998

PRIOR APPLICATION NUMBER: 60/146,222

PRIOR FILING DATE: July 28, 1999

PRIOR APPLICATION NUMBER: PCT/US98/19330

PRIOR FILING DATE: September 16, 1998

PRIOR APPLICATION NUMBER: PCT/US98/25108

PRIOR FILING DATE: December 1, 1998

PRIOR APPLICATION NUMBER: 09/216,021

PRIOR FILING DATE: December 16, 1998

PRIOR APPLICATION NUMBER: 09/218,517

PRIOR FILING DATE: December 22, 1998

PRIOR APPLICATION NUMBER: 09/254,311

PRIOR FILING DATE: March 3, 1999

PRIOR APPLICATION NUMBER: PCT/US99/12252

PRIOR FILING DATE: June 22, 1999

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: September 15, 1999

PRIOR APPLICATION NUMBER: PCT/US99/28409

PRIOR FILING DATE: No. US20020110859A1

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: No. US20020110859A1

PRIOR APPLICATION NUMBER: PCT/US99/28301

PRIOR FILING DATE: December 1, 1999

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: December 16, 1999

PRIOR APPLICATION NUMBER: PCT/US00/03565

PRIOR FILING DATE: February 11, 2000

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: February 22, 2000

PRIOR APPLICATION NUMBER: PCT/US00/05841

PRIOR FILING DATE: March 2, 2000

PRIOR APPLICATION NUMBER: PCT/US00/08439

PRIOR FILING DATE: March 30, 2000

PRIOR APPLICATION NUMBER: PCT/US00/14042

PRIOR FILING DATE: May 22, 2000

PRIOR APPLICATION NUMBER: PCT/US00/20710

PRIOR FILING DATE: July 28, 2000

PRIOR APPLICATION NUMBER: PCT/US00/32678

PRIOR FILING DATE: December 1, 2000

PRIOR APPLICATION NUMBER: PCT/US01/06520

PRIOR FILING DATE: February 28, 2001

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 61

LENGTH: 440

TYPE: PRT

ORGANISM: Homo Sapien

US-09-944-457-61

Query Match 99.1%; Score 2263; DB 9; Length 440;

Best Local Similarity 99.5%; Pred. No. 3.8e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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QY 1 MASVYVLSGSGCAAAAAAAPPGLRLLLLLPSAALLFTGCGNLFYDVTVIGEVA 60
Db 1 MASVYVLSGSGCAAAAAAAPPGLRLLLLLPSAALLFTGCGNLFYDVTVIGEVA 58
QY 61 TISQVVKSDSDSVQILNPNRQTYFPDPRPLKDSRFQNLNFSSELKSLTVNSISDQ 120
Db 59 TISQVVKSDSDSVQILNPNRQTYFPDPRPLKDSRFQNLNFSSELKSLTVNSISDQ 118
QY 121 RYFQOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCNAMSKATTTIRNF 180
Db 119 RYFQOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCNAMSKATTTIRNF 178
QY 181 KGNTELKGSKEVEWMSDMYVTSQMLKVKHEDDGVVICQVHPATVGLQFORLIEVQ 240
Db 179 KGNTELKGSKEVEWMSDMYVTSQMLKVKHEDDGVVICQVHPATVGLQFORLIEVQ 238
QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEALGKPOVMTVWVYVDEMPQHAVLSGNLFI 300
Db 239 YKPOVHIQMTYPLQGLTREGDALELTCEALGKPOVMTVWVYVDEMPQHAVLSGNLFI 298
QY 301 NNLKNTNGTGRCAASNVGKASDVMLYYDPEPTTIPPETTTTTTTTTTTTTTTT 360
Db 299 NNLKNTNGTGRCAASNVGKASDVMLYYDPEPTTIPPETTTTTTTTTTTTTTTT 358
QY 361 SRAGESSIRAVDAVIGVAVVVFAMLCILLIGRYFARHKQYFTHERAKGADADA 420
Db 359 SRAGESSIRAVDAVIGVAVVVFAMLCILLIGRYFARHKQYFTHERAKGADADA 418
QY 421 DTALINNEGQNNSEKKEYFI 442
Db 419 DTALINNEGQNNSEKKEYFI 440
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RESULT 13

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US-09-944-862-61
; Sequence 61, Application US/09944862
; Patent No. US20020115145A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavith, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACTDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,862
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
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; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
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; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
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; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020115145A1e1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020115145A1e1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO: 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-862-61
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Query Match 99.1%; Score 2263; DB 9; Length 440;

Best Local Similarity 99.5%; Pred. No. 3,8e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Db 1 MASVLPBGSQCAAAAAAAPPGL--LRLLLLLFSAALIPFGDQNLPTKDVVIEGEVA 58
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Db 59 TISCVNNSDDSVIQLNPNQOTYFRPRLKDSRQOLNFSSELKXSLTNVSIISDEG 118
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Db 119 RYFCQLYTPDPOESYTTITVLVPPRNLMID:QKDTAAGEBIEVNCJAMASKPATITRMF 178
OY 161 KGNTEIKGKSEVEEMSDMYTTSQMLKVHKEDGVPICQVEHPATYGNLQTORYLEVQ 240
Db 179 KGNTEIKGKSEVEEMSDMYTTSQMLKVHKEDGVPICQVEHPATYGNLQTORYLEVQ 238
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Db 239 YKPOVHICMTYPLQGLTREGDALEITCEALGKPOVWVWTVRVDDENPCHAVLSGPRLFI 298
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Db 299 NNKTKDNGTYRCASNVGSAHSDYMLVYDPTTTPPTTTTTTTTTTTTTTTTTTTTT 358
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Db 359 SRAGEGSIKRAVDNAVIGVAVVFMALCLITLGRFARHKGYTFTHAKGADDA 418
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Db 419 DTAILINAEQGQNNSEKKEKYEPI 440

RESULT 14
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/ Patent No. US20020127643A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Botstein, David
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gerritsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul
/ APPLICANT: Grimaldi, Christopher
/ APPLICANT: Gunney, Austin
/ APPLICANT: Hillman, Kenneth
/ APPLICANT: Kljavin, Ivar
/ APPLICANT: Napier, Mary
/ APPLICANT: Roy, Margaret
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Wood, William
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P2548P1C1
/ CURRENT APPLICATION NUMBER: US/09/945,587
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: 09/866,028
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/067,411
/ PRIOR FILING DATE: December 3, 1997
/ PRIOR APPLICATION NUMBER: 60/069,334
/ PRIOR FILING DATE: December 11, 1997
/ PRIOR APPLICATION NUMBER: 60/069,335
/ PRIOR FILING DATE: December 11, 1997
/ PRIOR APPLICATION NUMBER: 60/069,278
/ PRIOR FILING DATE: December 11, 1997
/ PRIOR APPLICATION NUMBER: 60/069,425
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/ PRIOR FILING DATE: December 12, 1997
/ PRIOR APPLICATION NUMBER: 60/069,696
/ PRIOR FILING DATE: December 16, 1997
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/ PRIOR FILING DATE: December 16, 1997
/ PRIOR APPLICATION NUMBER: 60/069,702
/ PRIOR FILING DATE: December 16, 1997
/ PRIOR APPLICATION NUMBER: 60/069,870
/ PRIOR FILING DATE: December 17, 1997
/ PRIOR APPLICATION NUMBER: 60/069,873
/ PRIOR FILING DATE: December 17, 1997
/ PRIOR APPLICATION NUMBER: 60/068,017
/ PRIOR FILING DATE: December 18, 1997
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/ PRIOR FILING DATE: January 5, 1998
/ PRIOR APPLICATION NUMBER: 60/074,086
/ PRIOR FILING DATE: February 9, 1998
/ PRIOR APPLICATION NUMBER: 60/074,092
/ PRIOR FILING DATE: February 9, 1998
/ PRIOR APPLICATION NUMBER: 60/075,945
/ PRIOR FILING DATE: February 25, 1998
/ PRIOR APPLICATION NUMBER: 60/112,850
/ PRIOR FILING DATE: December 16, 1998
/ PRIOR APPLICATION NUMBER: 60/113,296
/ PRIOR FILING DATE: December 22, 1998
/ PRIOR APPLICATION NUMBER: 60/146,222
/ PRIOR FILING DATE: July 28, 1999
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/ PRIOR FILING DATE: December 1, 1998
/ PRIOR APPLICATION NUMBER: 09/216,021
/ PRIOR FILING DATE: December 16, 1998
/ PRIOR APPLICATION NUMBER: 09/218,517
/ PRIOR FILING DATE: December 23, 1998
/ PRIOR APPLICATION NUMBER: 09/254,311
/ PRIOR FILING DATE: March 3, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/12252
/ PRIOR FILING DATE: June 22, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: September 15, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/28409
/ PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/28301
/ PRIOR FILING DATE: December 1, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: December 16, 1999
/ PRIOR APPLICATION NUMBER: PCT/US00/03565
/ PRIOR FILING DATE: February 11, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: February 22, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/05841
/ PRIOR FILING DATE: March 2, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/08439
/ PRIOR FILING DATE: March 30, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/14042
/ PRIOR FILING DATE: May 22, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/20710
/ PRIOR FILING DATE: July 28, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/32678
/ PRIOR FILING DATE: December 1, 2000
/ PRIOR APPLICATION NUMBER: PCT/US01/06520
/ PRIOR FILING DATE: February 28, 2001
/ NUMBER OF SEQ ID NOS: 120
/ SEQ ID NO 61
/ LENGTH: 440
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-945-587-61
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Query Match

99.1%; Score 2263; DB 9; Length 440;

Best Local Similarity 99.5%; Pred. No. 3.8e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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DB 1 MASVTVSSGSCAAAAAAPP--LRLLLLFSAAALFTGGQQLFTDVTVIGEVA 58
QY 61 TISQVVKSDSDSVIQLNPNRQRTYFRDPRPLKDSRFQNLNFSSELKXSLTNVSI SDG 120
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DB 179 KGNTELKGSKEVEWMSMTYTSQMLKVKKEDDGVAVICQVHPAVTGNLQTORLEVQ 238
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DB 239 YKPOVHIQMTYPLQGLTREGDAILTCEAIGKQPPVMTWVRVDEMPQHAVLSGNLFT 298
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DB 299 NNLMKTNGTGRCAASNIIVGKASDVMLYYDPTTTPPTTTTTTTTTTTTTTTTT 358
QY 361 SRAGEGSIKRAVDHVTGGVAVVVFAMLCILLIGFYFARHKQTYFTHAKGADADA 420
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DB 419 DTALINAEQGNSEKKEVEFI 440
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US-09-945-015-61
Sequence 61, Application US/09945015
Patent No. US20020132768A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Batstein, David
APPLICANT: Bacon, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Gettitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/945,015
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
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PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
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PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
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PRIOR APPLICATION NUMBER: 60/074,092
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PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
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PRIOR APPLICATION NUMBER: PCT/US00/05841
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PRIOR APPLICATION NUMBER: PCT/US00/08439
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PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-945-015-61
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Query Match 99.1%; Score 2263; DB 9; Length 440;

Best Local Similarity 99.5%; Pred. No. 3.8e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Db	179	KGNTLKGKSEVEEMSDMTTTSQMLKVKHKKDDGVVICQVEHPAVTGNLQTORYLEVQ	238
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QY	361	SRAGEEGSIRAVDHAIVGGVAVVFAVLCILLIGRYFARHKGTFTHEAKGADDAADA	420
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CM protein - protein search, using sw model

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637.949 Million cell updates/sec

Title: US-10-622-237-2

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2283	100.0	442	4	US-09-930-803-1 Sequence 1, App1
3	2263	99.1	440	4	US-09-866-028-61 Sequence 61, App1
4	2169	95.0	423	4	US-09-778-510-22 Sequence 22, App1
5	902	39.5	444	2	US-08-658-984A-5 Sequence 5, App1
6	902	39.5	444	3	US-08-660-531-5 Sequence 5, App1
7	895.5	39.2	421	2	US-08-658-984A-1 Sequence 1, App1
8	895.5	39.2	421	3	US-08-660-531-1 Sequence 1, App1
9	745.5	32.7	398	4	US-03-778-510-4 Sequence 4, App1
10	739	32.4	398	4	US-03-778-510-6 Sequence 6, App1
11	739	32.4	398	4	US-09-907-794A-84 Sequence 84, App1
12	739	32.4	398	4	US-09-905-125A-84 Sequence 84, App1
13	739	32.4	398	4	US-09-902-755A-84 Sequence 84, App1
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15	335	11.7	517	4	US-09-723-368-4 Sequence 947, App1
16	256.5	11.2	518	4	US-09-723-368-4 Sequence 4, App1
17	248	10.9	518	4	US-09-919-172-20 Sequence 20, App1
18	232	10.2	393	1	US-08-429-742-2 Sequence 2, App1
19	226	9.9	479	4	US-09-723-368-2 Sequence 2, App1
20	222	9.7	458	4	US-09-435-956A-1 Sequence 1, App1
21	220.5	9.7	344	4	US-03-700-387-3 Sequence 3, App1
22	211	9.2	313	4	US-03-700-397-3 Sequence 4, App1
23	208	9.1	388	1	US-08-429-742-4 Sequence 4, App1
24	206	9.0	642	1	US-08-217-299-1 Sequence 1, App1
25	206	9.0	698	2	US-08-602-725-36 Sequence 36, App1
26	206	9.0	734	2	US-08-389-459A-17 Sequence 17, App1
27	206	9.0	734	3	US-08-987-867A-17 Sequence 17, App1

28	205.5	9.0	338	4	US-09-976-594-404 Sequence 404, App
29	205.5	9.0	1461	4	US-09-576-594-531 Sequence 531, App
30	200.5	8.8	308	2	US-08-414-657D-46 Sequence 46, App1
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36	199.5	8.7	338	2	US-09-135-080-4 Sequence 4, App1
37	199.5	8.7	1241	3	US-09-040-774-2 Sequence 2, App1
38	199	8.7	582	4	US-09-702-705-334 Sequence 334, App
39	199	8.7	582	4	US-09-736-457-334 Sequence 334, App
40	199	8.7	582	4	US-09-614-124B-334 Sequence 334, App
41	199	8.7	582	4	US-09-671-325-334 Sequence 334, App
42	199	8.7	582	4	US-09-589-184-334 Sequence 334, App
43	198.5	8.7	335	2	US-08-414-657D-47 Sequence 47, App1
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ALIGNMENTS

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Sequence 20, Application US/09778510									
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GENERAL INFORMATION:									
APPLICANT: Baum, Peter									
TITLE OF INVENTION: Molecules Designated B7L1									
FILE REFERENCE: 2844-US									
CURRENT APPLICATION NUMBER: US/09/778,510									
CURRENT FILING DATE: 2001-02-07									
PRIOR APPLICATION NUMBER: PCT/US99/17906									
PRIOR FILING DATE: 1999-08-05									
PRIOR APPLICATION NUMBER: 60/095,663									
PRIOR FILING DATE: 1998-08-07									
NUMBER OF SEQ ID NOS: 22									
SOFTWARE: Patent In Ver. 2.0									
SEQ ID NO 20									
LENGTH: 442									
TYPE: PRT									
ORGANISM: Homo sapien									
US-09-778-510-20									
Query Match									
Best Local Similarity 100.0%; Score 2283; DB 4; Length 442;									
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MASVLPSSGSCAAAAA	PPGLRLRLILFSAALIP	TDGQNLFTKDYTVT	EGEVA	60			
DB	1	MASVLPSSGSCAAAAA	PPGLRLRLILFSAALIP	TDGQNLFTKDYTVT	EGEVA	60			
QY	61	TISCCVKNKDDSVIQLN	PNRQTIYFRDPRPKDSR	FQLNPSSELKYSI	INVSISDBG	120			
DB	61	TISCCVKNKDDSVIQLN	PNRQTIYFRDPRPKDSR	FQLNPSSELKYSI	INVSISDBG	120			
QY	121	RFFCQLYTDPDES	YTTITVLVPPNNMID	IKDTAVGEEIEVNC	TAAASRPATTIRWF	180			
DB	121	RFFCQLYTDPDES	YTTITVLVPPNNMID	IKDTAVGEEIEVNC	TAAASRPATTIRWF	180			
QY	181	KNGTEIKGSEVEE	MSDYTVTSQMLKVKH	KEDDGVPI	COVEHFAVNGN	OTORYLEVO	240		
DB	181	KNGTEIKGSEVEE	MSDYTVTSQMLKVKH	KEDDGVPI	COVEHFAVNGN	OTORYLEVO	240		
QY	241	YRPQVHIQNTYPL	QGLTREGDLEITCE	AIKQPKQPVMTW	RVDDMPQHAVL	SGPNLFI	300		
DB	241	YRPQVHIQNTYPL	QGLTREGDLEITCE	AIKQPKQPVMTW	RVDDMPQHAVL	SGPNLFI	300		
QY	301	NNLNTKDNSTVRC	EASNTVIGKASHDY	MYVVDPTTIP	PTTTTITTTTIT	ITTTTITTTT	360		
DB	301	NNLNTKDNSTVRC	EASNTVIGKASHDY	MYVVDPTTIP	PTTTTITTTTIT	ITTTTITTTT	360		

QY 361 SRAGEGSIKAVDAHVIGVAVVVFAMCLIIILGRYFARHKGTYFTHAKADADA 420
Db 361 SRAGEGSIKAVDAHVIGVAVVVFAMCLIIILGRYFARHKGTYFTHAKADADA 420
QY 421 DTAINAEGGONNSEKKEYFI 442
Db 421 DTAINAEGGONNSEKKEYFI 442

RESULT 2

US-09-930-803-1
Sequence 1, Application US/09930803
Patent No. 6596493
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: REEVES, Roger
APPLICANT: YOSHINORI, Muzumaki
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILE REFERENCE: JUL1770-1
CURRENT APPLICATION NUMBER: US/09/930,803
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 442
TYPE: PRT
ORGANISM: Homo sapiens
US-09-930-803-1

Query Match 100.0%; Score 2283; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 6,6e-192;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPESGSCCAAAAAAAPPGLRLRLLLLFSAALIFPGDONLFTKDVYVIEBEVA 60
Db 1 MASVLPESGSCCAAAAAAAPPGLRLRLLLLFSAALIFPGDONLFTKDVYVIEBEVA 60
QY 61 TISCVNKSDDSVIQLNPNRQTIYFRDFRPLKDSRFQOLNFSSELKVSITNVSISDEG 120
Db 61 TISCVNKSDDSVIQLNPNRQTIYFRDFRPLKDSRFQOLNFSSELKVSITNVSISDEG 120
QY 121 RYFCQLYTDPQESYTTITVLPVRNLMIDIQKOTAVGEEIEVNCAMASKPATITRMF 180
Db 121 RYFCQLYTDPQESYTTITVLPVRNLMIDIQKOTAVGEEIEVNCAMASKPATITRMF 180
QY 121 RYFCQLYTDPQESYTTITVLPVRNLMIDIQKOTAVGEEIEVNCAMASKPATITRMF 180
Db 121 RYFCQLYTDPQESYTTITVLPVRNLMIDIQKOTAVGEEIEVNCAMASKPATITRMF 180
QY 181 KNTLKGSEVEEWSMDVYITVSQMLKVHKEDDGVPIQVHEPAVTGNLQOTRYLEVO 240
Db 181 KNTLKGSEVEEWSMDVYITVSQMLKVHKEDDGVPIQVHEPAVTGNLQOTRYLEVO 240
QY 241 YKPOVHIOMTYPLQGLTREGDALBELTCEAIGKPOVWVTVWRVDDEMPQHAVLSGPNLFI 300
Db 241 YKPOVHIOMTYPLQGLTREGDALBELTCEAIGKPOVWVTVWRVDDEMPQHAVLSGPNLFI 300
QY 301 NNKNTDNGTYRCEASNIVGKASHDYMLYVDPPTTIPPTTTTTTTTTTTTTTTTT 360
Db 301 NNKNTDNGTYRCEASNIVGKASHDYMLYVDPPTTIPPTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKAVDAHVIGVAVVVFAMCLIIILGRYFARHKGTYFTHAKADADA 420
Db 361 SRAGEGSIKAVDAHVIGVAVVVFAMCLIIILGRYFARHKGTYFTHAKADADA 420
QY 421 DTAINAEGGONNSEKKEYFI 442
Db 421 DTAINAEGGONNSEKKEYFI 442

RESULT 3

US-09-866-028-61
Sequence 61, Application US/09866028
Patent No. 6642360
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David

APPLICANT: Baton, Dan
APPLICANT: Perrata, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavira, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tomas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2549P1
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult PAM or file wrapper
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-866-028-61

Query Match 99.1%; Score 2263; DB 4; Length 440;
Best Local Similarity 99.5%; Pred. No. 3,7e-190;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MASVLPESGSCCAAAAAAAPPGLRLRLLLLFSAALIFPGDONLFTKDVYVIEBEVA 60
Db 1 MASVLPESGSCCAAAAAAAPPGLRLRLLLLFSAALIFPGDONLFTKDVYVIEBEVA 58
QY 61 TISCVNKSDDSVIQLNPNRQTIYFRDFRPLKDSRFQOLNFSSELKVSITNVSISDEG 120
Db 59 TISCVNKSDDSVIQLNPNRQTIYFRDFRPLKDSRFQOLNFSSELKVSITNVSISDEG 118
QY 121 RYFCQLYTDPQESYTTITVLPVRNLMIDIQKOTAVGEEIEVNCAMASKPATITRMF 180
Db 119 RYFCQLYTDPQESYTTITVLPVRNLMIDIQKOTAVGEEIEVNCAMASKPATITRMF 178
QY 181 KNTLKGSEVEEWSMDVYITVSQMLKVHKEDDGVPIQVHEPAVTGNLQOTRYLEVO 240
Db 179 KNTLKGSEVEEWSMDVYITVSQMLKVHKEDDGVPIQVHEPAVTGNLQOTRYLEVO 238
QY 241 YKPOVHIOMTYPLQGLTREGDALBELTCEAIGKPOVWVTVWRVDDEMPQHAVLSGPNLFI 300
Db 239 YKPOVHIOMTYPLQGLTREGDALBELTCEAIGKPOVWVTVWRVDDEMPQHAVLSGPNLFI 298
QY 301 NNKNTDNGTYRCEASNIVGKASHDYMLYVDPPTTIPPTTTTTTTTTTTTTTTTT 360
Db 299 NNKNTDNGTYRCEASNIVGKASHDYMLYVDPPTTIPPTTTTTTTTTTTTTTTTT 358
QY 361 SRAGEGSIKAVDAHVIGVAVVVFAMCLIIILGRYFARHKGTYFTHAKADADA 420
Db 359 SRAGEGSIKAVDAHVIGVAVVVFAMCLIIILGRYFARHKGTYFTHAKADADA 418
QY 421 DTAINAEGGONNSEKKEYFI 442
Db 419 DTAINAEGGONNSEKKEYFI 440

RESULT 4

US-09-778-510-22
Sequence 22, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510

CURRENT FILING DATE: 2001-02-07
 PRIOR APPLICATION NUMBER: PCT/US99/17906
 PRIOR FILING DATE: 1999-08-05
 PRIOR APPLICATION NUMBER: 60/095,663
 PRIOR FILING DATE: 1996-08-07
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: Patent Ver. 2.0
 SEQ ID NO: 22
 LENGTH: 423
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-778-510-22

Query Match 95.0%; Score 2169; DB 4; Length 423;
 Best Local Similarity 98.8%; Pred. No. 6,1e-182;
 Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

QY 19 AAPPGLRLRLLLFFSAAALIPDGGQVLFKDVYIEGEVATISQVKNSSDDSVIQLLN 78
DB 1 AAPPGLRLRLLLISAAALIPDGGQVLFKDVYIEGEVATISQVKNSSDDSVIQLLN 60
QY 79 PNRQTIYFRDPRPKDSRFQLLNFSSSELKVSLTNVSISSDEGRYFCQLYTDPQESYTTI 138
DB 61 PNRQTIYFRDPRPKDSRFQLLNFSSSELKVSLTNVSISSDEGRYFCQLYTDPQESYTTI 120
QY 139 TLVLPNRLMTDQKQDAVEGEIEIVNCTAMASKPATIRFKKNTLKGKSEVEEWSDM 198
DB 121 TLVLPNRLMTDQKQDAVEGEIEIVNCTAMASKPATIRFKKNTLKGKSEVEEWSDM 180
QY 199 YTVTSQMLKVKHKEDDGVFVICOVEHPAVTGNLTQRYLEVOYKPOVHIQMTYPLQGLTR 258
DB 181 YTVTSQMLKVKHKEDDGVFVICOVEHPAVTGNLTQRYLEVOYKPOVHIQMTYPLQGLTR 240
QY 259 BGDALETCEAIGRQPVMTWVAVDDMPQHAVLSGPNLPINNLTNDNGTYRCEASNT 318
DB 241 BGDALETCEAIGRQPVMTWVAVDDMPQHAVLSGPNLPINNLTNDNGTYRCEASNT 300
QY 319 VGKASHDYMXYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTTDSAGEGSIKAVDAVIG 378
DB 301 VGKASHDYMXYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTTDSAGEGSIKAVDAVIG 360
QY 379 GVAVAVVVFAMCLIIIGRYFARHKGYFTHEAKGADDAADADTAIINAEQGNNSSEKK 438
DB 361 GVAVAVVVFAMCLIIIGRYFARHKGYFTHEAKGADDAADADTAIINAEQGNNSSEKK 420
QY 439 EYF 441
DB 421 EYF 423
  
```

RESULT 5
 US-08-659-984A-5
 Sequence 5, Application US/08659984A
 Patent No. 5943400
 GENERAL INFORMATION:
 APPLICANT: Anderson, John P.
 APPLICANT: Simha, Sukanto
 APPLICANT: Jacobson-Croak, Kirsten L.
 TITLE OF INVENTION: Assays for Detecting Beta-Secretase
 TITLE OF INVENTION: Inhibition
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Ctr., 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/659,984A
 FILING DATE: 07-JUN-1996
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/485,152
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Haslin, James M.
 REGISTRATION NUMBER: 29,541
 REFERENCE/DOCKET NUMBER: 15270-002810US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 444 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-659-984A-5

Query Match 39.5%; Score 902; DB 2; Length 444;
 Best Local Similarity 44.6%; Pred. No. 8.3e-71;
 Matches 194; Conservative 74; Mismatches 137; Indels 30; Gaps 7;

```

QY 31 LIFSAAA---LIPDGGQVLFKDVYIEGEVATISQVKNSSDDSVIQLLNPNRQTIYFR 87
DB 17 LIFSAAA---LIPDGGQVLFKDVYIEGEVATISQVKNSSDDSVIQLLNPNRQTIYFR 76
QY 88 DFRPLKDSRFQLLNFSSSELKVSLTNVSISSDEGRYFCQLYTDPQESYTTITVLVPPNLL 147
DB 77 DFRPLKDSRFQLLNFSSSELKVSLTNVSISSDEGRYFCQLYTDPQESYTTITVLVPPNLL 136
QY 148 MIDIQKDAVEGEIEIVNCTAMASKPATIRFKKNTLKGKSEVEEWS---DMYTVTSQ 204
DB 137 QISGSSPVMEGDMQLCTKTSKSPRADIRFKKNTLKGKSEVEEWS---DMYTVTSQ 196
QY 205 LMLKVKHKEDDGVFVICOVEHPAVTGNLTQRYLEVOYKPOVHIQMTYPLQGLTRREGAL 263
DB 197 LDFRDRSDSDGVAVICRDHESLNATPQVAVLEIHTPEKTI---IPSTFPPEGQPL 253
QY 264 ELTCAIGRQPVMTWVAVDDMPQHAVLSGPNLPINNLTNDNGTYRCEASNTYK 321
DB 254 ILTCSKKGKPEPEVLTWTKDGEPLDPRMVSGRLEMLPLNKTNDNGTYRCEASNTYK 313
QY 322 AHSDFWLYVYDPTTTPPTTTTTTTTTTTTTTTTTTTTTDSAGEGSIKAVDAVIG 367
DB 314 AHSDFWLYVYDPTTTPPTTTTTTTTTTTTTTTTTTTTTDSAGEGSIKAVDAVIG 373
QY 368 STRAVDAVIGVAVVVFAMCLIIIGRYFARHKGYFTHEAKGADDAADADTAIINA 427
DB 374 P---DHALIGGIYVAVVVFILCSIFLGRYLARHKGYFTHEAKGADDAADADTAIINA 429
QY 428 EGGQNNSEKKEKYEYF 442
DB 430 EGGQNNSEKKEKYEYF 444
  
```

RESULT 6
 US-08-660-531-5
 Sequence 5, Application US/08660531
 Patent No. 6221645
 GENERAL INFORMATION:
 APPLICANT: Chrysler, Susanna M.S.
 APPLICANT: Simha, Sukanto
 APPLICANT: Keim, Pamela S.
 APPLICANT: Anderson, John P.
 TITLE OF INVENTION: Beta-Secretase
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-531-5

Query Match
Best Local Similarity 39.5%; Score 902; DB 3; Length 444;
Matches 194; Conservative 74; Mismatches 137; Indels 30; Gaps 7;

31 LIFSA--LIFGDNLFKQVTVIEGVAISQVNSDVSQILNPNRQTIYR 87
17 LLLAAAKNKVKSQGGFLTONVTVGGTALITCRVDNDNTSLQSNPAQOTLYFD 76
88 DFRPKDSRFLNLSSELKVSLSNVISDEGRYFCOLYDPPQESYTTITVLPNNIL 147
77 DKKALRDRRIELVRASWHELSISVDSLSDEGQYCSLTMPVKSKALTYLVGPEKP 136
148 MIDQKDAVEGELEVNCTAMASKPATITRMFKGNTLKGKSEVEWS---DMYTVTSQ 204
137 QISGSSVPMEGDLQILCTKTSKSPADIRWFNDKEIKDVYKKEEDANRKTFTVSSST 196
205 LMLKVKHEDDGVPIVQVEHPAVTGNLQ--TORYLEVQYKPOVHIQMTYPLQGLTREGDAL 263
197 LDFRDRSDGVAIVCRVDHESLNATPOVAMQVLEHNTSVKI---IPSTFPQGGPL 253
264 ELTCATGKPOVATYWRVDDEM--POHAYLSGPNLFINNKTNDNGTYRCAASIVTK 321
254 ILTCSKSKPLPEPILMTKDGELPDPDRVVSRELNILFNKTDNGTYRCAATYIQ 313
322 AHSYMLVYDPTTPTPTT 367
314 SSAEVLIVHVPNTLPTTIIIPSLTATVTTVAITTSPTTSATISSIRDPNALAGQNG 373
368 SIRAVDAVIGVAVVVFAMLCILITLGRYPARHKTYTTHKAGDADADATIAINA 427
374 P---DHALIGGIYAVVFTLCSIFLGRYLAHKGYTLINAKGADPADATIAINA 429
428 EGGQNNSEKKEFYI 442
430 EGGQVNAEKEKEFYI 444

RESULT 7
US-08-659-984A-1
Sequence 1, Application US/08659984A

Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Creack, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-1

Query Match
Best Local Similarity 45.1%; Score 895.5; DB 2; Length 421;
Matches 189; Conservative 73; Mismatches 130; Indels 27; Gaps 6;

44 GONLFTQVTVIEGVAISQVNSDVSQILNPNRQTIYRDFRPKDSRFLNLS 103
10 GQPLTONVTVGGTALITCRVDNDNTSLQSNPAQOTLYFDKKALRDRRIELVRAS 69
104 SSELKVSLSNVISDEGRYFCOLYDPPQESYTTITVLPNNIMIDQKDAVEGELE 163
70 WHELSISVDSLSDEGQYCSLTMPVKSKALTYLVGPEKPOLISGSSVPMEDLQ 129
164 VNCTAMASKPATITRMFKGNTLKGKSEVEWS---DMYTVTSQILMLKVKHEDDGVPIVC 220
130 LITCTSKSKPADIRWFNDKEIKDVYKKEEDANRKTFTVSSSTLDFRDRSDGVAIVC 189
221 QVEHPATVGNLQ--TORYLEVQYKPOVHIQMTYPLQGLTREGDALELTCATGKPOVWMT 279
190 RVHDESINATPOVAMQVLEHNTSVKI---IPSTFPQGGPLILTCSKSKPLPEPVL 246
280 WVRVDDEM--POHAYLSGPNLFINNKTNDNGTYRCAASIVGKAHSDYMLVYDPTTI 337
247 WTKGQGLPDPDRVVSRELNILFNKTDNGTYRCAATNTIGQSSAEVLLIVHVPNTL 306
338 PPTTT 383
307 LPTIIIPSLTATVTTVAITTSPTTSATISSIRDPNALAGQNG---DHALIGGIYAV 362
384 VVFAMLCILITLGRYPARHKTYTTHKAGDADADATIAINAEGQNNSEKKEFYI 442


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/ APPLICANT: Baum, Peter
/ TITLE OF INVENTION: Molecules Designated B711
/ FILE REFERENCE: 2844-US
/ CURRENT APPLICATION NUMBER: US/09/778,510
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: PCT/US99/17906
/ PRIOR FILING DATE: 1999-08-05
/ PRIOR APPLICATION NUMBER: 60/095,663
/ PRIOR FILING DATE: 1998-08-07
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO: 6
/ LENGTH: 398
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-778-510-6

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Query Match 32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1.4e-56;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps 9;

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QY 22 PGLRLRLILFLSAAALIPG----DQNLFTKDVTVIEGEVATISQVKNKSDSVYQL 76
DB 4 PASALLLLLLF-ACCMAPGAGNISQDDSPMTSDETVVAGTVVLCQVQDHDSDSLQW 62
QY 77 LNPNRQTIYFRDPRPLKDSRFOLNFSSELKVLTVNVSIDEGRYFCOLYTDPPQESYT 136
DB 63 SNPAQGTLYFGSKRLRDRNRQIVTSTPHLSISINVALADEGEYTCISIFMPVTRAKS 122
QY 137 TITVLYPPRLMIDIQKTAIVEGEIEVNCYTAASKPATITIRKGNTEIKK-SEVEEM 195
DB 123 LVTVLGIQKPIITGYKSSIREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIOED 182
QY 196 SD--MYVTSQLMLKHKEDDGVPIQVEHPATG-NLQTORLEQYKQVHIQWTP 252
DB 189 PDKFTVYSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLVPTMIRDP 242
QY 253 LOGLRREGDALELTEALGKQKQPVVTVVRVDDEMPCHAVLSCNLFINNANTDNGTTR 312
DB 243 --HPRQKQLLHREGNVPQOYIMK-EGSVPLKQTESALIFPLNKSQGTG 298
QY 313 CEASNIYKASDYLIVYDPTTLPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 372
DB 299 CATSNMGSYKAYVILNNDPS---PVSSSSSTY----- 329
QY 373 DNVAIVGVVAVVFMCLLILIGRYFARKGTYFTTHANGADADADADATATINAGGON 432
DB 330 -HAITGGIVAFVFLILMLIFLGHYILRHKGTYLTHKAGSDADPADTAIINAGGOS 388
QY 433 NSEKKEEYFI 442
DB 389 GGDDEKKEFYI 398

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RESULT 11

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US-09-907-794A-84
/ Sequence 84, Application US/0907794A
/ Patent No. 6635468

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GENERAL INFORMATION:

```

/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fond, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gettleisen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.

```

```

/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth, J.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paonli, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William, I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: 10466-14
/ CURRENT APPLICATION NUMBER: US/09/907,794A
/ PRIOR FILING DATE: 2001-07-17
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: US 60/143,048
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: US 60/145,698
/ PRIOR FILING DATE: 1999-07-26
/ PRIOR APPLICATION NUMBER: US 60/146,222
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: PCT/US99/20594
/ PRIOR FILING DATE: 1999-09-08
/ PRIOR APPLICATION NUMBER: PCT/US99/20944
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/21547
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/23089
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: PCT/US99/28214
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: 1999-11-30
/ PRIOR APPLICATION NUMBER: PCT/US99/28564
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO: 84
/ LENGTH: 398
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-907-794A-84

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Query Match 32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1.4e-56;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps 9;

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QY 22 PGLRLRLILFLSAAALIPG----DQNLFTKDVTVIEGEVATISQVKNKSDSVYQL 76
DB 4 PASALLLLLLF-ACCMAPGAGNISQDDSPMTSDETVVAGTVVLCQVQDHDSDSLQW 62
QY 77 LNPNRQTIYFRDPRPLKDSRFOLNFSSELKVLTVNVSIDEGRYFCOLYTDPPQESYT 136
DB 63 SNPAQGTLYFGSKRLRDRNRQIVTSTPHLSISINVALADEGEYTCISIFMPVTRAKS 122
QY 137 TITVLYPPRLMIDIQKTAIVEGEIEVNCYTAASKPATITIRKGNTEIKK-SEVEEM 195
DB 123 LVTVLGIQKPIITGYKSSIREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIOED 182

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RESULT 12
US-09-905-125A-84
; Sequence 84, Application US/09905125A
; Patent No. 6664376
; Journal: TUNISIEN

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsens, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumans, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acid Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089

ORGANISM: Homo sapiens
US-09-905-1125A-84

Query Match	32.4%;	Score 739;	DB 4;	Length 398;
Best Local Similarity	38.6%;	Pred. No. 1.4e-56;		
Matches 166;	Conservative 73;	Mismatches 147;	Indels 44;	Gaps 9

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QY      2  PGRLRLILLLESAALIPTG---DQNLFTKDVTVIEGEVATISQVNVKSDSYIOL  76
Db      4  PASLLILLILLF-ACCMARGANISQSDSQEMPTSDIETVAGIYVLKQCVQDHEDSSIQW  62
QY      77  LNPENRTIYFRDPRFLPKSRFOLLNFSSELEKVSILTVNISISEGRYFCOLYTPDEPQESYT  136
Db      63  SNAQOQTLTFYGEKRALRDNRILQLVSTPHELTISISNVLADEGEYICSIETWVRFAKS  122
QY      137  TTVLTPPPNMLIDIQXONTAVEGEIEVMTCTMAASKPATTTIRWKKGTMLKG-SEVEEW  195
Db      123  LTVLIGIPKXPITTIYKSSLRKQDTATLNCSSSKSPARLTWRKKGOEHLGHEPTRIOED  182
QY      196  SD--MYTVTSQMLKVNKEDDGVPIVCQVHEPAATG-NLQRYLEVOYKQVHIQMTYP  252
Db      183  PGNKFTVYSSVTFQVTRREDDGASIVCSVNHESLKGDRISSQIEVLVYPTAMIRDP  242
QY      253  LOGLRREDDALETTEAIGKFPQVMTWRVDDEMPHAVISGENLEINNLTNDGTGR  312
Db      243  --HPRREGKLLHCEGRGNFVPOQYIMEX-EGSVPLKMTQESALIFPLNLSDSGTYG  298
QY      313  CEASNIYVGAHSDWMLYYVDPETTTTPPTTTTTTTTTTTTTTTTTLIIIDSAAGEGSIKAV  372
Db      299  CTRATSMGSYKAYITLANNDPS---PVPSSSTY-----  329
QY      373  DHAVTGVAAVVVPAMLCLIIIGRYPARHGIYFTHEAKGADDAADATAIINAEGGN  432
Db      330  -HAIGGIYAVFVFLIIMLIFLGHYLIRKHGTYLTHEAKGSDPADADATAIINAEGGS  368
QY      433  NSEKKEEYFI  442
Db      389  GGDGDKKEEYFI  398

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RESULT 13
 US-09-902-775A-84
 Sequence 84, Application US/09902775A
 Patent No. 6686451
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 APPLICANT: Asitkrazhi, Avi
 APPLICANT: Bostein, David
 APPLICANT: Bostemiers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Neptoleme
 APPLICANT: Filvaroff, Ellen

```

APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-08-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-775A-84

Query Match
Best Local Similarity 32.4%; Score 739; DB 4; Length 398;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps 9;

QY 22 PGLRLRLILFSAALIPFG-----DQGNLFTQDVIVIGEVATISCOVNSKSDSVIQL 76
DB 4 PAASILLILLLF-ACCMAPGAGANLSQDDSQPWSDETIVAGGVIVLKCQVXKHEDSSLSLW 62
QY 77 LNPNGQITVFPDPRPLKDSRFPQLNLFSSSELKXSLTNVSSISDEGRYFCQLYTPDPQESY 136

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DB 63 SNPAQQLTYFGEKALNDNRQLVTSRPHLSISISVALADEGETCSIFTPVPTAKS 122
QY 137 TITVIVPPRNIMIDIOQDVAEGEIEVNTAASAPATIRPKNTLEKGR-SEVERM 195
DB 123 LVTVGLTIPKPIITGVYSREKNTATLNQSSGSKPAALTRKDDQLHGPRTIQD 182
QY 186 SD--MYVTSQLMKVHKEDGVVICOVEPAVVG-NLQTORVLEVOYKPCVHIQMTVP 252
DB 183 PNGKFTVSSSVTFQVREDGASIVCSVNHESIKGADRSQRIEVLVTPFAMIRPDP 242
QY 253 LOGLTREDALELCEALCKPQPMVTVAVDDEMQHVALSPNLFINNLTNDGTR 312
DB 243 --HPRBSQKLLHCBGRGNVPQOYIWEK-EGSVPLKQTSALIFPLKNSDSGTG 298
QY 313 CEASNVKASNDYMLVYDPPITPTITTTTTTTTTTTTTTTTTITDSRAGEGSIKAV 372
DB 299 CTATSNMGSYKAYVTLVNDPS--PVSSSTY----- 329
QY 373 DHAVIGGVAVVPPAMCLIIIGRYPARHKGTVFTHKAGDADADATATINAGGON 432
DB 330 -HAIIGIVAFIVFLHMLFIHGYLIRKGYTLTHKAGSDADADATATINAGGOS 388
QY 433 NSEKKEYFI 442
DB 389 GDDKKEYFI 398

RESULT 14
US-09-778-510-2
Sequence 2, Application US/0978510
Patent No. 6512095
GENERAL INFORMATION:
APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 432
TYPE: PRT
ORGANISM: Homo sapien
US-09-778-510-2

Query Match
Best Local Similarity 31.6%; Score 722; DB 4; Length 432;
Matches 169; Conservative 74; Mismatches 143; Indels 78; Gaps 11;

QY 22 PGLRLRLILFSAALIPFG-----DQ-----ONT----- 47
DB 4 PAASILLILLLF-ACCMAPGAGANLSQDGYWQEDDELGTIADLDAISSTVSSPDMLAS 62
QY 48 -----FTKQVTVIEGEVATISCOVNSKSDSVIQLNPNKQITVFPDPRPLKDSRFPQLNLF 102
DB 63 QDSQPWTSDETIVAGGVIVLKCQVXKHEDSSLSLWNSPAAQQLTYFGEKALRNRLQLVTS 122
QY 103 SSSELKXSLTNVSSISDEGRYFCQLYTPDPQESYTTITVIVPPRNIMIDIOQDVAEGEIE 162
DB 123 TPEHLISISISVALADEGETCSIFTPVPTAKSLVTVLGIQKPIITGVYSLSREKDTA 182
QY 163 EVNCTAASAPATIRPKNTLEKGR-SEVERMSD--MYVTSQLMKVHKEDGVVICOVEPA 219
DB 183 TLNCGSSGKPAALTRKDDQLHGPRTIQDPRNGKFTVSSSVTFQVREDGASIV 242
QY 220 CQVHEPAVVG-NLQTORVLEVOYKPCVHIQMTVPLOGLTREDALELCEALCKPQPMV 278
DB 243 CSVNHESIKGADRSQRIEVLVTPFAMIRPDP--HPRBSQKLLHCBGRGNVPQOY 299

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QY 279 TWAVDEMPQCHAVLSGNLFINNINLKTNDGTYRCEASNIYKHAHSDYMLVYDPTTIP 338
DB 300 LWEX-EGSVPLKMQSALIFPFLNKSDSGTYGTATSNMGSYAYTTLVNDPS--P 355
QY 339 PPTTTTTTTTTTTTTTTTTIIIDSRAGEGSIKAVDAVIGVAVVYFAMLCIIIGRY 398
DB 356 VPSSTSY-----HAIIGIVAFIVFLLIMLIFIGHY 388
QY 399 FAHKGTYFTEHAKGADDAADATTAIINAEAGGONNSEKKEVEI 442
DB 389 LIRHKGTYLTHAKSDAPADDTAIIINAEAGGSGDDKXEYFI 432

RESULT 15
US-09-205-258-947
; Sequence 947, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373

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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
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; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
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; EARLIER APPLICATION NUMBER: 60/048,974
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; EARLIER APPLICATION NUMBER: 60/048,883
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
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; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 947
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-947

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Query Match          14.7% Score 335; DB 4; Length 227;
Best Local Similarity 33.8%; Pred. No. 1,66-21;
Matches 78; Conservative 48; Mismatches 97; Indels 8; Gaps 5;

QY 106 ELKVSILNVSIDSEGRYFCQLYTDPQESYTTITVLPBRLMTDIOQTAVEGEIEVN 165
DB 1 ELISISNVALADEGEYTCISIFTEVTRAKSIVTVLGIPKPIITGYKSSLRKDTATLN 60

QY 166 CTAMASKPATITRMKGNTELKXK-SEVEEMSD--MYVTQOLMKYHAKEDDGVVITQV 222
DB 61 CGSSGSKRAARLTWRKGOELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDQASIVCSV 120

QY 223 EHPAVTG-NLQORYLEVQYKPOVAHIQMTYPLQGLTRGDALLETCEAIGKQPFVMVTV 281
DB 121 NHESLKADRSITSGIEVLYPTLMIRBDP--HPRRGQTLHCBORGKPFVQOQYIME 177

QY 282 RVDDEMPQCHAVLSGNLFINNINLKTNDGTYRCEASNIYKHAHSDYMLVYD 332
DB 178 K-EGSVPLKMQSALIFPFLNKSDSGTYGTATSNMGSYAYTTLVND 227

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Job time : 37.7688 secs

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C:/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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R:Sulston, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19355
A:Accession: T20992
A:Status: preliminary; translated from GB/EMBL/DBD
A:Residues: 1-5175 <MIL>
A:Molecule type: DNA
A:Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:FL5G9.4a
A:Experimental source: clone F15G9
R:Kershaw, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24734
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-5175 <M12>
A:Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:FL5G9.4a
A:Experimental source: clone T09B9
C:Genetics: F15G9.4a
A:Map position: X
A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
A:Exons: 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
A:Introns: 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1;
A:Exons: 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1;
Query Match 11.9%; Score 261.5; DB 2; Length 5175;
Best Local Similarity 24.6%; Pred. No. 1.1e-09;
Matches 87; Conservative 65; Mismatches 130; Indels 71; Gaps 15;
Qy 34 VTVEGEVATISCCVNSDSDSVIQLNPNRQTYFRDPRP---KDSRFQNLNFSSEL 89
Db 2200 VTAIKGALPFRKCID--DDK---NFKGQIIMLRNYQCIDLEADARITRL---SND 2249
Qy 90 KVSILTNVISDEGRYFCOLYTDPPQESYT-TITVLPVRNLMIDIQD-TAVGESEIEN 147
Db 2250 RLTIINTVNDGEGYSCRKXNDAGENSFDFKATLVPTTLMIDKXKTAHVSHSTVLS 2309
Qy 148 CTAASKPATITIRPFKG-----NKLKSKSEVEEWSMDYVTSQMLKVKH 193
Db 2310 CPA-TGKREPITTFKGEAHIENADIENGILNG-----NQLKITRIK 2354
Qy 194 EDDGVPIVQVHPAVTGNLTQRYLYEVQKPOVH---IQWYLPQGLTREGDAFELTCE 250
Db 2355 EGDAGKYTCEDANS--GSVEODVNVVITIPKIEKDGIPSDYSQ---QNERVVISCP 2408
Qy 251 AIGKQPMVMTWVRVDEMPQHAVL---SGPNLFNNLKTNDGTYRCEASNIYGRAS 306
Db 2409 VYARP-PAKITWLAKGKPLQSDKFKVKSANGQKLYLFKLKETSSTKTCIATNAGDKR 2467
Qy 307 DYMVYVDPPTTTP-----PTTTTTTTTTTTTTTTTTDSRAGE 347
Db 2468 DFKVSMVAFPDEBNIVRITVNSGNPSTLHCPAKGSPPTITWLKGNALIE 2520
RESULT 3
T43290
hemiscentin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text change 18-Feb-2000
C:Accession: T43290; T20993; T24734
R:Voegel, B.B.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1996
A:Description: Hemiscentin is required for hemidesmosome mediated cell adhesion and germ
A:Reference number: Z22396
A:Accession: T43290
A:Molecule type: RNA
A:Residues: 1-5198 <VOG>
A:Cross-references: EMBL:AF074901; PIDN:AA026792.1
R:Sulston, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19355
A:Accession: T20993

A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-5198 <MIL>
A:Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:FL5G9.4b
A:Experimental source: clone F15G9
R:Kershaw, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24734
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-5198 <M12>
A:Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:FL5G9.4b
A:Experimental source: clone T09B9
C:Genetics: hlm-4; F15G9.4b
A:Map position: X
A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
A:Exons: 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
A:Introns: 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1;
A:Exons: 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1;
Query Match 11.9%; Score 261.5; DB 2; Length 5198;
Best Local Similarity 24.6%; Pred. No. 1.1e-09;
Matches 87; Conservative 65; Mismatches 130; Indels 71; Gaps 15;
Qy 34 VTVEGEVATISCCVNSDSDSVIQLNPNRQTYFRDPRP---KDSRFQNLNFSSEL 89
Db 2200 VTAIKGALPFRKCID--DDK---NFKGQIIMLRNYQCIDLEADARITRL---SND 2249
Qy 90 KVSILTNVISDEGRYFCOLYTDPPQESYT-TITVLPVRNLMIDIQD-TAVGESEIEN 147
Db 2250 RLTIINTVNDGEGYSCRKXNDAGENSFDFKATLVPTTLMIDKXKTAHVSHSTVLS 2309
Qy 148 CTAASKPATITIRPFKG-----NKLKSKSEVEEWSMDYVTSQMLKVKH 193
Db 2310 CPA-TGKREPITTFKGEAHIENADIENGILNG-----NQLKITRIK 2354
Qy 194 EDDGVPIVQVHPAVTGNLTQRYLYEVQKPOVH---IQWYLPQGLTREGDAFELTCE 250
Db 2355 EGDAGKYTCEDANS--GSVEODVNVVITIPKIEKDGIPSDYSQ---QNERVVISCP 2408
Qy 251 AIGKQPMVMTWVRVDEMPQHAVL---SGPNLFNNLKTNDGTYRCEASNIYGRAS 306
Db 2409 VYARP-PAKITWLAKGKPLQSDKFKVKSANGQKLYLFKLKETSSTKTCIATNAGDKR 2467
Qy 307 DYMVYVDPPTTTP-----PTTTTTTTTTTTTTTTTTDSRAGE 347
Db 2468 DFKVSMVAFPDEBNIVRITVNSGNPSTLHCPAKGSPPTITWLKGNALIE 2520
RESULT 4
HLMSP3
poliovirus receptor homolog precursor - mouse
C:Species: Mus musculus domesticus (western European house mouse)
C:Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text change 22-Jun-1999
C:Accession: A38211
R:Morrison, M.E.; Raccanelli, V.R.
J. Virol. 66, 2807-2813, 1992
A:Title: Molecular cloning and expression of a murine homolog of the human poliovirus re
A:Reference number: A38211; MUID:92219365; PMID:1560525
A:Accession: A38211
A:Molecule type: DNA
A:Residues: 1-467 <MOR>
A:Cross-references: GB:M80206; MUID:9199785; PIDN:AAA39734.1; PID:9199786
A:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: duplication; glycoprotein; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <Sig>
F:26-467/Product: poliovirus receptor homolog #status predicted <MAT>
F:26-354/Domain: extracellular #status predicted <EXT>
F:47-133/Domain: immunoglobulin homology <IMM1>
F:167-231/Domain: immunoglobulin homology <IMM2>
F:267-322/Domain: immunoglobulin homology <IMM3>
F:355-374/Domain: transmembrane #status predicted <TMN>

F:375-467/Domain: intracellular #status predicted <INT>
 F:54-131,174-229,274-320/Dissulfide bonds: #status predicted
 F:128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.2%; Score 246.5; DB 1; Length 467;
 Best Local Similarity 21.6%; Pred. No. 6e-10; Indels 99; Gaps 16;
 Matches 101; Conservative 72; Mismatches 196;

```

QY 4 PGLRLRLILLISAAALIPFGDQNLFTKDYVIEGEV---ATISQV-----48
DB 14 PTLPLPLILLL-----LQETG-AQDVRAVLPVWGRGLGVELPCHLLPPTERVSGVT 68
QY 49 -NKSDSVIQLNPNRQITFRDFRPLKDSRFQ-----LNFSSSLKVSILTNVIS 99
DB 69 WQRLDGVVAAPHB-----FGVDFPNSQFSKORLSFVARPBTADLDATLAFRGRLVE 124
QY 100 DEGRYFCQLYTP--PQESYTTITLVPPRNIMIDIQDTAVEGEIEV-----NCT 149
DB 125 DEGNVTCFATFPNGTRRGVTLRLVIAQEN-----HAHQVLTIGQSVAVARCV 175
QY 150 AMASRPATIRWFKG-NKELKGSVEEWSMDYVTSQMLKVHKEDDGVPIQVEHPA 208
DB 176 STGGPPPARITWISLGEBAQDTPFGIOAGVTIISRYSLVPYGRADGVAVTCRVEHS 235
QY 209 VTGNLQTRYLEVQYKPVNHIQMTYPLQGLTRBGDAFELTCEALGKQPVWVTVWRVDE 266
DB 236 FEEPIILPVTLISVRYPEVIS--GYDDNWYIGRSEAI-LTCDVANSNEPDTYDKSTSGV 293
QY 269 MPQHAVLSGPNLFNNLKTNGTYRCEASNIVGKASDVMLYVYDPTTIPPTTTT 328
DB 294 FPASAVAGSQLVHVSVRMNTTIFICTATNAVGTGABQVILVRDTPQA-----343
QY 329 TTTTTLTTLITTSRAGEEGTIGAVDHAIVGVAVVVR--MLCLIIIGRFYHKG 386
DB 344 -----SR-----DVGPLWGAAGVGLLVLLAGGFLAILLRGRRRRSPG 384
QY 387 TYFHEAKGADA-----ADADTAIINAGGQNNSEKKE 421
DB 385 GGGNDGGRGSYDPKTYQVNGGPGVFWMSASPEPRPRGREDDEEEEBE 432

```

RESULT 5

poliovirus receptor-related protein precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
 C/Accession: J04024
 R/Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubn
 Gene 155, 261-265, 1995
 A/Title: Complementary DNA characterization and chromosomal localization of a human gene
 A/Reference number: J04024; MUID:95237621; PMID:7721102
 A/Accession: J04024
 A/Molecule type: mRNA
 A/Residues: 1-518 <LOP>
 A/Cross-references: EMBL:X76400; NID:9732795; PIDN:CAA53960.1; PID:9732796
 C/Genetics:
 A/Gene: GDB:PVRR1
 A/Cross-references: GDB:583951
 A/Map position: 11q23-11q24
 C/Superfamily: poliovirus receptor; immunoglobulin homology
 C/Keywords: glycoprotein; transmembrane protein
 F:1.30/Domain: signal sequence #status predicted <SIG>
 F:31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
 F:36-379/Domain: transmembrane #status predicted <TM>
 F:36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.1%; Score 244; DB 2; Length 518;
 Best Local Similarity 25.1%; Pred. No. 1e-09;
 Matches 104; Conservative 59; Mismatches 155; Indels 96; Gaps 20;

```

QY 56 IQLNPNRQITFRDFRPLKDSRFQNLNFSSELKVSILTNVISIDEGRYFCQLYTPP--113
DB 78 VAIYNPBMGVSVLAPYR-----ERYEFLRPSFTDGTIRLSRLLEDEGVYICBATPPTGN 133

```

```

QY 114 QESYTTITLVPPRNIMIDIQD-TAVEGEIEV---NCTAMASRPATIRWFKGNKELK 169
DB 134 RESQMLNLTWAKRPTNMIIEGQAVLRAKQGDQDKVAVATCSANGKPSVSV--ETRLK 190
QY 170 GKSEV--EWSMD--YTTSQMLKVHKEDDGVPIQVEHPAVTGNLQTRY-----LE 220
DB 191 GEARVPDGSCTPMAPTVVISRYELVPSREAHQOQSLACIV-----NYHMRKESILTIN 243
QY 221 VQYKPVNHIQ--MTVPLQGLTRBGDAFELTCEALGKQPVWVTVWRVDEMPQHAVLSG 277
DB 244 VQTEPEVTLIEGFGNWTYLRMD-----VKLTCAADANPPATEYHMTTLNGSLPKVEAON 298
QY 278 PNLFINN-LNKTDNGTYRCEASNIVGKASDVMLYVYDPTTIPPTTTTTTTTTTTT 336
DB 299 RTLFFKGPINYSLAGYICEDATNPIDTRSGQVEVNTERTPIRPSF-----344
QY 337 LTIITSRAGEEG-TIGAVDHAIVGVAVVVR--MLCLIIIGRFYHKG--RH--KGYTF 389
DB 345 -----EHGRRAPVPTAIIIGVAGSI--LVLIVVGGIIVALLRRRHTEFGDYS 391
QY 390 T-----HEAKGA-----DDAADATAIINAGGQNNSEKKE 421
DB 392 TKKHVYGNNGSKAGIQHHPRPAQNLYRPDDSDDEKKA--GLDGSYSIEEEEBE 443

```

RESULT 6

poliovirus receptor mpvr - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
 C/Accession: A53437
 R/Aoki, U.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
 J. Biol. Chem. 269, 8431-8438, 1994
 A/Title: Amino acid residues on human poliovirus receptor involved in interaction with
 A/Reference number: A53437; MUID:94179228; PMID:8132669
 A/Accession: A53437
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-530 <NOX>
 A/Cross-references: GB:ID26107; NID:9475017; PIDN:BA05103.1; PID:9825507
 A/Experimental source: C57/BL6, brain
 A/Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBI:146667)
 C/Superfamily: poliovirus receptor; immunoglobulin homology
 F:47-133/Domain: immunoglobulin homology <IM>

Query Match 11.1%; Score 243; DB 2; Length 530;
 Best Local Similarity 22.6%; Pred. No. 1.2e-09;
 Matches 90; Conservative 61; Mismatches 162; Indels 86; Gaps 14;

```

QY 4 PGLRLRLILLISAAALIPFGDQNLFTKDYVIEGEV---ATISQV-----48
DB 14 PTLPLPLILLL-----LQETG-AQDVRAVLPVWGRGLGVELPCHLLPPTERVSGVT 68
QY 49 -NKSDSVIQLNPNRQITFRDFRPLKDSRFQ-----LNFSSSLKVSILTNVIS 99
DB 69 WQRLDGVVAAPHB-----FGVDFPNSQFSKORLSFVARPBTADLDATLAFRGRLVE 124
QY 100 DEGRYFCQLYTP--PQESYTTITLVPPRNIMIDIQDTAVEGEIEV-----NCT 149
DB 125 DEGNVTCFATFPNGTRRGVTLRLVIAQEN-----HAHQVLTIGQSVAVARCV 175
QY 150 AMASRPATIRWFKG-NKELKGSVEEWSMDYVTSQMLKVHKEDDGVPIQVEHPA 208
DB 176 STGGPPPARITWISLGEBAQDTPFGIOAGVTIISRYSLVPYGRADGVAVTCRVEHS 235
QY 209 VTGNLQTRYLEVQYKPVNHIQMTYPLQGLTRBGDAFELTCEALGKQPVWVTVWRVDE 266
DB 236 FEEPIILPVTLISVRYPEVIS--GYDDNWYIGRSEAI-LTCDVANSNEPDTYDKSTSGV 293
QY 269 MPQHAVLSGPNLFNNLKTNGTYRCEASNIVGKASDVMLYVYDPTTIPPTTTT 328
DB 294 FPASAVAGSQLVHVSVRMNTTIFICTATNAVGTGABQVILVRDTPQA-----343

```

Oy 329 TTTTTLITITDSRAGEGTIGAVDHVIGVAVV 367
 Db 344 -----AGAGATG-----ITGGIATAT 361

RESULT 7

168093
 PRR2 delta - human
 C:Species: Homo sapiens (man)
 C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
 C:Accession: 168093
 R:Berle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
 Gene 159, 267-272, 1995
 A:Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th
 A:Reference number: 153960; MUID:95347610; PMID:7622062
 A:Accession: 168093
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-538 <RES>
 A:Cross-references: GB:579172; NID:g1042204; PID:g1042205
 C:Genetics:
 A:Gene: PRR2delta
 C:Superfamily: poliovirus receptor; immunoglobulin homology
 F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 10.8%; Score 238.5; DB 2; Length 538;

Best Local Similarity 22.8%; Pred. No. 2, 6e-09; Mismatches 196; Indels 113; Gaps 17;

Matches 110; Conservative 63; Mismatches 196; Indels 113; Gaps 17;

Oy 2 APPGLRLILLLSAALIPITGQGNLFKDVTVIEGEVATISCVNKSDDSVIQLNP 61
 Db 12 SPFLPLMLPILLL-----LLETG-AQDVRYQVLPEVFG-----QLGTVELPCILLP 59
 Oy 62 -----NRQTYFRDPRPKDSRF-----QLNFSSS----- 87
 Db 60 VPGYISLVTVQRDAPANQNV--AAFHPRMGSPSPKRGSERLSPVSAKOSTGQDTE 117
 Oy 88 -----ELKVSILNVSISDEGRYFCQLYTDP--PQESYTTITVLVPPRLMIDIQKTAVEG 141
 Db 118 AELDQATLALHGLTVEDEGNVTCFATFPKGSVRGTMVIAKPKA-QAEAKVTFPSQD 176
 Oy 142 EEIEVNCITANASKPATITRFKQ-NKELKGSVEEMSDMTVTSQMLKVKHEDGVY 200
 Db 177 PTVVALGISKRGPRAPISWLSLMDWAKETQVSGTLGAVTVTSRPTLVPSGRADGVTV 236
 Oy 201 ICQVHNRAVGNLQTVRYLEVQYKQVHIQMTYVLOGLTREGAFELTCEAIKQPVWV 260
 Db 237 TCKVHESFEPPALIIVTLVRYRPEVVIS-GIDDMVYLCRTD--TLSCDVRSNPEPTG 294
 Oy 261 TWVVDDEMPQHAVLSGPNLFNNIKTNGTYACEASNIVGKAHSDYMLVYVDPPTIIP 320
 Db 295 DMSITSGTFPSNAQSQSLVIAVNDLFTTFCVTNVAVGGRAGQVIFVRETPRT-- 352
 Oy 321 PPTTTTTTTTTTTTTLITITDSRAGEGTIGAVDHVIGVAVVFAFMCILLIGRY 380
 Db 353 -----AGAGATG-----ITGGIATATATAATGILICR 383
 Oy 381 FARKGTFTHEAKGADDAADAD-----TAIINAE-----GGONNSEKKE 421
 Db 384 QQRKEQT-----LQAEHEDDLBGRPSYKPTPRKAKLEAQMPSQLFTLQASHSPKTP 438
 Oy 422 YF 423
 Db 439 YF 440

RESULT 8

JE0099
 cell adhesion molecule 1 - African clawed frog
 N:Alternate names: N-CAM 1
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: JE0099
 R:Kudo, M.; Takayama, E.; Tadakuma, T.; Shikawa, K.
 Biochem. Biophys. Res. Commun. 245, 127-132, 1998
 A:Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-Cams) as the ma
 A:Reference number: JE0099; MUID:98204770; PMID:9535795

A:Accession: JE0099

A:Molecule type: mRNA

A:Residues: 1-725 <KID>

A:Cross-references: DBJ:AB008162; NID:g3116226; PID:NBA25931.1; PID:g3116227

A:Experimental source: heart

C:Comment: This protein mediates and regulates various cell-cell interactions through bo

C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

F:413-475/Domain: immunoglobulin homology <IMM>

F:512-589/Domain: fibronectin type III repeat homology <FR>

Query Match 10.8%; Score 238; DB 2; Length 725;
 Best Local Similarity 26.2%; Pred. No. 4, 2e-09;
 Matches 89; Conservative 61; Mismatches 148; Indels 42; Gaps 15;

Oy 32 KDVTVIEGEVATISC---QVN---KSDDSVLIQLN---PNRQTYFRDPRPKDSRFQ 81
 Db 139 KDIQVIVNVPPPTIQARQLRVNATKMAESVLSGDAQGFDPDELISWIKKEPIEDGB-EX 257
 Oy 82 LNFSSSELKVSILNVSISDEGRYFCQLYTDPQESYTTITVLVPPRLMIDIQKTAVEG 141
 Db 258 ISFNEDQSEMTIHHVEKXDEAEVSC-IANNQAGEAEATILIKYAKEXITVVENKTAVAL 316
 Oy 142 EEIEVNCITANASKPATITRFKQKKE-----LKGSVEEMSDMTVTSQMLKVKHE 194
 Db 317 DEITLTCEA-SGDIPSTIWTAVRANISSEKTTIDGHIYKHEIRM-----SALTLDIQY 371
 Oy 195 DDGVAVICQVHNRAVGNLQTVRYLEVQYKQVHIQMTYVLOGLTREGAFELTCEAIK 254
 Db 372 TDAGEYFCIANP-IGVDMQAM-YFEVQYAKIR-----GPVAVYTWEGNPNVITCEVFAH 425
 Oy 255 PQVWNTVTRVDDMPQH-----AVLSGP---NFNNIKTNGTYACEASNIVGKAH 306
 Db 426 PR-AAVTFWRDQQLPSSNFNISKIYSGPISSSLEVVPDSNDGYNCTALINTIGHEFS 484
 Oy 307 DMLVYVDPPTIIPPTTTTTTTTTTTTTTTTTLITITDSRAG 346
 Db 485 EPIVQADTPSS---PAIRKPEPSSYTWIYFDDPDDTGG 521

RESULT 9

A44194
 poliovirus receptor (clone AGM-alpha-1) - green monkey
 C:Species: Cercopithecus aethiops (green monkey, grivet)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: A44194
 R:Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotch, O.; Nomoto, A.
 J. Virol. 66, 7059-7066, 1992
 A:Title: A second gene for the African green monkey poliovirus receptor that has no put
 A:Reference number: A44194; MUID:93059651; PMID:1331508
 A:Accession: A44194
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-417 <KOI>
 A:Cross-references: GB:S48777
 C:Superfamily: poliovirus receptor; immunoglobulin homology
 C:Keywords: transmembrane protein
 F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 10.8%; Score 237; DB 2; Length 417;
 Best Local Similarity 23.8%; Pred. No. 2, 4e-09;
 Matches 107; Conservative 68; Mismatches 194; Indels 80; Gaps 18;

Oy 1 APPGLRLILLLSAALIPITGQGNLFKDVTV--IEGEVATISC--QVNSDSDSVI 56
 Db 8 AMPF-----LLTTLLELSWPPPGDIIIVAGPQVPEFLDSTVLPCLVPGMEETHV 61
 Oy 57 QLINPVR-----QTYFRDPRPKDSRFQLNFSSELKVSILNVS-----ISDERY 104

```

Db      62 SOLTMRHSGSGMAVHQTGPNYSEPRLEFVARLCTELRDASLIMFGLRVDEGNY 121
QY      105 FQQLYDDPQESYTT---ITVVPRLNIMIDOKTAVEGEIEY-NCTAMASKPATITR 160
Db      122 TC-LFTVFPQGRSDIMLRVLAKEPN-TAEVOK-VOLTGKRPVAVRCSVSGRPAHIT 178
QY      161 WFKGNKEKLGKSEVE---WSDMTVTYSQMLTKYHKEKDDGPVVCQVEHPAVTGNLQTO 216
Db      179 W---HSDLGMPNTOQAPGFLSGYTVTSMLTVSSQVDGKSVTCYKHEHSEFKPQLLT 235
QY      217 RYLEVQYKPOVHIQMTYPLQGLTREGDAFELTCEAIKGPQVMTVWVDEMPQAVLS 276
Db      236 VMLTYVYPPPEVVIS-GYDNMWYLSQNEA-TLTCDAKSNDEPFGYMWSTMGPLPFAVAQ 293
QY      277 GPNLNNLNKTDNCTYCEASNIYKKAHSDMYLVYVDPPTIIPPTTTTTTTTTTTTTT 336
Db      294 GQQLIRPYDKPINTTFCNVTNALGARQAEITLVQKGPPEPS----- 338
QY      337 LTIITDSRAGEGTIGAVDHAIVGVAVVFMCLIIILGRYPARKGT-----YFTHE 392
Db      339 -----GMSNNIIFILIGIVI---LTLTIGIVYFRRCRREFLMCHHL 380
QY      393 AKGADDAADADTAITNABGQNNSEKKE 421
Db      381 SPSSEHASA-----SANGYISYSDVSR 404

```

RESULT 10

```

B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C/Spectes: Cercopithecus aethiops (green monkey, givret)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: B44194
R/Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotroh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A/Title: A second gene for the African green monkey poliovirus receptor that has no puta
A/Reference number: A44194; MUID:93059651; PMID:1331508
A/Accession: B44194
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-392 <KOI>
A/Cross-references: GB:S48817
C/Superfamily: poliovirus receptor; immunoglobulin homology
F:259-314/Domain: immunoglobulin homology <IMM>

```

```

Query Match      10.7%; Score 234.5; DB 2; Length 392;
Best Local Similarity 24.4%; Pred. No. 3.4e-09;
Matches 100; Conservative 58; Mismatches 180; Indels 71; Gaps 16;

```

```

QY      1 AAPGLRLRLILLLLSAALPTGQNLFTKQTV--IEGEVATISC--QVNSKDSQVI 56
Db      8 AMP-----LTLTLELSWPPPGTGDITVQAPQVPGFLDSDVTLPCYLQVPMEEHTV 61
QY      57 QLNENR-----QTIYFRDPRPLKDSRFQLNFSSELKYSILTVS-----ISDEGRY 104
Db      62 SOLTMRHSGSGMAVHQTGPNYSEPRLEFVARLCTELRDASLIMFGLRVDEGNY 121
QY      105 FQQLYDDPQESYTT---ITVVPRLNIMIDOKTAVEGEIEY-NCTAMASKPATITR 160
Db      122 TC-LFTVFPQGRSDIMLRVLAKEPN-TAEVOK-VOLTGKRPVAVRCSVSGRPAHIT 178
QY      161 WFKGNKEKLGKSEVE---WSDMTVTYSQMLTKYHKEKDDGPVVCQVEHPAVTGNLQTO 216
Db      179 W---HSDLGMPNTOQAPGFLSGYTVTSMLTVSSQVDGKSVTCYKHEHSEFKPQLLT 235
QY      217 RYLEVQYKPOVHIQMTYPLQGLTREGDAFELTCEAIKGPQVMTVWVDEMPQAVLS 276
Db      236 VMLTYVYPPPEVVIS-GYDNMWYLSQNEA-TLTCDAKSNDEPFGYMWSTMGPLPFAVAQ 293
QY      277 GPNLNNLNKTDNCTYCEASNIYKKAHSDMYLVYVDPPTIIPPTTTTTTTTTTTTTT 336
Db      294 GQQLIRPYDKPINTTFCNVTNALGARQAEITLVQKGPPEPS----- 338

```

```

QY      337 LTIITDSRAGEGTIGAVDHAIVGVAVVFMCLIIILGRYPARK 385
Db      339 -----GMSNNIIFILIGIVI---LTLTIGIVYFRSR 369

```

RESULT 11

```

LUXNL
neural cell adhesion molecule long domain form precursor - African clawed frog
N/Alternate names: NCAM-180
N/Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C/Spectes: Xenopus laevis (African clawed frog)
C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C/Accession: S09600
R/Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Acids Res. 17, 10321-10335, 1989
A/Title: Primary structure and developmental expression of a large cytoplasmic domain f
A/Reference number: S09600; MUID:90098871; PMID:2481269
A/Accession: S09600
A/Molecule type: mRNA
A/Residues: 1-1088 <XRI>
A/Cross-references: EMBL:M5696; NID:g214609; PID:AAA49909.1; PID:g214610
A/Note: the authors translated the codon AAA for residue 970 as Leu
C/Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mc
C/Genetics: Several forms of NCAM are produced by alternative splicing.
A/Genes: NCAM
C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; im
C/Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <I
F:20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status pr
F:20-705/Domain: extracellular #status predicted <EXT>
F:34-95/Domain: immunoglobulin homology <IMM1>
F:129-188/Domain: immunoglobulin homology <IMM2>
F:149-153/Region: heparin binding #status predicted
F:158-162/Region: heparin binding #status predicted
F:225-284/Domain: immunoglobulin homology <IMM3>
F:317-381/Domain: immunoglobulin homology <IMM4>
F:413-475/Domain: immunoglobulin homology <IMM5>
F:512-569/Domain: fibronectin type III repeat homology <FN3>
F:618-679/Domain: fibronectin type III repeat homology <FN3B>
F:706-723/Domain: fibronectin type III repeat homology <FN3B>
F:724-1088/Domain: intracellular #status predicted <INT>
F:41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F:219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

```

Query Match      10.7%; Score 234; DB 1; Length 1088;
Best Local Similarity 25.9%; Pred. No. 1.3e-08;
Matches 88; Conservative 62; Mismatches 148; Indels 42; Gaps 15;

```

```

QY      32 KDVTVEGEVATISC---QVNS---DSEVIQLN-----PNQTIYFRDPRPLKDSRFQ 81
Db      199 KDQIVLVNVPPTIQARQLRVNATAMNASEVLSGADGPPDEISLTKGGEPIEDE-EK 257
QY      82 LNFSSSELKYSILTVSISDEGRFCQLYTDPQESTTTITVAVPRLNIMIDOKTAVUG 141
Db      258 ISFNEQSEWTHHVKDEDAEYSC-IANNQGEAATILKRYAPKITYENKTAVAL 316
QY      142 EEEVENCTAMASKPATITWPKGNKE-----LKKSEVEEMSDYATYSQMLKVKHE 194
Db      317 DEITLICEA-SGDPISITMTRAVRNISEATLDOHIVKHIR-----SALTLDIOY 371
QY      195 DQGVPIVCQVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTREGDAFELTCEAIK 254
Db      372 TDAGEYFCIASNP-IGVDQAM-YEVOYAPKIR---GPVVVYTWEGNPVAVITGEVFAH 425
QY      255 PCPVMTVWVAVDEMPQH-----AVISGP---NLFINLNKTDNCTYCEASNIYKKAH 306
Db      426 PR-AATVTRDQGLLPSSNFSNIKIYSGTSSLEVNPESEDPFGNYCTAINTIGHERS 484
QY      307 DYMIVYVDPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 346
Db      485 EFTLVQADTPSS---PAIRKVEPSSSTWIVDEPDDSTG 521

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Db 242 YPEVVIS-GYDNMTLGONEA-TLTCARSNPEPTGINKSTMGPELPFAVAGQALLI 299
 QY 283 NNINKTNDGTCEASNIYGAHSDYMLVYDPPTTIPPTTTTITTTITTTITTD 342
 Db 300 RPVDKPIINTTLLICVNTNALGARQAEITVQKE-----GPPSHS----- 338
 QY 343 SRAGEGTIGANDHAVIGVAVVVFAMCLIIIGRF 381
 Db 339 -----GMSRNAILFLVIGLIVF---LILGLIGIVF 365

RESULT 14

neurotrophin - rat
 156551
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
 C/Accession: 156551
 R.Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J.L.
 J. Neurosci. 15, 2141-2156, 1995
 A/Title: Cloning of neurotrophin defines a new subfamily of differentially expressed neur
 A/Reference number: 156551; MUID:95198094; PMID:7891157
 A/Accession: 156551
 A/Status: Preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-344 <RES>
 A/Cross-references: EMBL:U16845; NID:G755184; PIND:AA67445.1; PID:G755185
 C/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi

Query Match 10.5%; Score 231; DB 2; Length 344;
 Best Local Similarity 26.2%; Pred. No. 5, 1e-09;
 Matches 85; Conservative 56; Mismatches 134; Indels 50; Gaps 15;

QY 10 LLLLLSAALIPFG-----DQGNLFTK---DYTVIEGEVATISQVNSDSDSVQLNPN 62
 Db 14 LVVSLRLFLVPTVPVPSGDATFPKAMDVTVYQGSATLRTCT--DNKRVTVAMLN 70
 QY 63 FQTI-YFRDFPLKDSRFLNFSSELKSLTNVSISEGRYFCQLYTD-PQESYTTI 120
 Db 71 RSTILYAGNDKWCDFRVLLSNLTQYSEIIONVDYDEGPTCSVOTDNHPTKSRVHL 130
 QY 121 TVLVPRRLMDIDQCTAV-EGEIEVNCTAMASKPATITRMFKNKELKSGSEVEKSD 179
 Db 131 IVQVSPK--IVEISSDISINEGNNISLTCLIA-TGPRPEPTVMRHISPKAVGFVSEDEYLE 187
 QY 180 MYTVTSQMLKVH---KEDDGVPIQCYEHPAVTGNLQTRYLEVOYKPOVHIQMTYPLQ 236
 Db 188 IGGITREOSGHEGASNDVAAPVRRYN-----VTVNPPTIS-----EAK 229
 QY 237 GL-TREGAFELTCEAIKPGQVMTVTVRVDDEMPQ-----HAYLSGNLFINNLN 286
 Db 230 GTGVFVGQKGTLCQCEASAVPS-AEFQMFKDKRLVEGKGVKVENRPLSLRTFF--NVS 266
 QY 287 KTDNGTYRCEASNIYGAHSDYMLY 311
 Db 287 EHDYGNITCVASNKLGHNASIMLF 311

RESULT 15

138346
 elastic titin - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
 C/Accession: 138346
 R.Labeit, S.; Kolmerer, B.
 Science 270, 293-296, 1995
 A/Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
 A/Reference number: A57430; MUID:96026330; PMID:7569978
 A/Accession: 138346
 A/Status: Preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-7962 <RES>
 A/Cross-references: EMBL:X90569; NID:G1017426; PIND:CAA62189.1; PID:G1017427
 C/Genetics:

A/Gene: GDB:TTN
 A/Cross-references: GDB:127867; OMIM:188840
 A/Map position: 2q31-2q31

Query Match 10.4%; Score 228.5; DB 2; Length 7962;
 Best Local Similarity 26.1%; Pred. No. 4e-07;
 Matches 80; Conservative 55; Mismatches 130; Indels 41; Gaps 13;

QY 35 TVIEGEVATISQVNSDSDSVIQ---LNL-----PNRTIYFRDPRPLKDSRFQNLNF 84
 Db 770 TVLDRIAPFTPTPLRVNDVAVNGTGRDLCKIGSLPMRVS-WFKQGEIYASDRIRIAP 828
 QY 85 SSELKSLTNVSISEGRYFCQLYTD-PQESYTTITVLVPPRNIMIDIQDTAVEGEE 143
 Db 829 VEGTASLEIRVMDNDAGNFTCRATNSVSGSKSSGALIVQEPSPFTKPSKD-VLPGSA 887
 QY 144 IEVNCTAMASKPATITRMFKNKELG-----KSEVEKSDMYTVTSQMLKVHKKEDD 196
 Db 888 VCLKSTFGSTP-LTRKMFKNKELVSGGSCYITKEALBSLELYLV-----KTSQ 937
 QY 197 GVPYICQVEHPAVTGNLQTRYLEVOYKPOVHIQMTYPLQGLTRGDAFELTCEAIKPGQ 256
 Db 938 SGTYTCVSN--VAGGVECSANLFLVK-EPATFVEXKLEPSQ-LKKGDATQLACKVTGTP- 992
 QY 257 PVAWTVVRVDDEMPQHA-----VLSGNLFINNLKTDNGTYRCEASNIYGAHSDYML 310
 Db 993 PKITWFAANDREIKESSKHMSFVESTAVRLTVDGIEDSGEYMCQAQNEAGSDHCSIV 1052
 QY 311 YVYDPP 316
 Db 1053 IVKESP 1058

Search completed: July 7, 2004, 06:00:28
 Job time: 33.2751 secs

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GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 ; Search time 27.874 Seconds

(without alignments)
790.187 Million cell updates/sec

Title: US-10-622-237-4

Perfect score: 2197

Sequence: 1 AAPPGLRLRLILLISAAAL.....TAIINAGQGNSEKKEYP 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	229.5	11.8	515	1	Q9G176 sus scrofa
2	252.5	11.5	517	1	PVR1_PIG
3	243	11.1	530	1	PVR2_MOUSE
4	238.5	10.9	538	1	PVR2_HUMAN
5	237	10.8	417	1	PVR_CERAE
6	236	10.7	515	1	PVR1_MOUSE
7	234	10.7	1088	1	NCA1_XENLA
8	232	10.6	344	1	NTR1_MOUSE
9	231.5	10.5	417	1	PVR_HUMAN
10	231	10.5	344	1	NTR1_RAT
11	229	10.4	344	1	NTR1_HUMAN
12	225.5	10.3	837	1	NCM2_MOUSE
13	222	10.1	837	1	NCM2_HUMAN
14	222	10.1	1092	1	NCA2_XENLA
15	221	10.1	1242	1	NPHN_MOUSE
16	220.5	10.0	338	1	LAMP_CHICK
17	220	10.0	337	1	OPCM_CHICK
18	218	9.9	583	1	OPCM_MOUSE
19	217.5	9.9	345	1	OPCM_BOVIN
20	215.5	9.8	345	1	OPCM_HUMAN
21	214	9.7	588	1	OPCM_CHICK
22	211	9.6	847	1	CD22_HUMAN
23	211	9.6	4391	1	PGEM_HUMAN
24	209.5	9.5	345	1	OPCM_HUMAN
25	209	9.5	353	1	CEPU_CHICK
26	207.5	9.4	509	1	SHS1_RAT
27	207.5	9.4	646	1	MUS1_HUMAN
28	207	9.4	1493	1	MUS1_MOUSE
29	206.5	9.4	338	1	LAMP_HUMAN
30	206.5	9.4	862	1	CD22_MOUSE
31	204.5	9.3	338	1	LAMP_RAT
32	204	9.3	702	1	CEAS_HUMAN
33	203.5	9.3	583	1	CI66_HUMAN

34	203	9.2	1461	1	NEO1_HUMAN	Q92859 homo sapien
35	202	9.2	1443	1	NEO1_CHICK	Q90610 gallus gall
36	198	9.0	1377	1	NEO1_RAT	P97603 rattus norv
37	197	9.0	3707	1	PGEM_MOUSE	Q05793 mus musculu
38	196.5	8.9	1241	1	NPHN_HUMAN	Q05000 homo sapien
39	196.5	8.9	1331	1	CTA2_HUMAN	Q9uh66 homo sapien
40	195	8.9	506	1	SHS1_BOVIN	Q46531 bos taurus
41	194	8.8	1091	1	NCA1_CHICK	P13590 gallus gall
42	193	8.8	761	1	NCA2_HUMAN	P13592 homo sapien
43	192.5	8.8	848	1	NCA1_HUMAN	P13591 homo sapien
44	192	8.8	1036	1	AXO1_CHICK	P28685 gallus gall
45	191.5	8.7	853	1	NCA1_BOVIN	P31836 bos taurus

ALIGNMENTS

RESULT 1	ID	SVR1_PIG	STANDARD	PRT	515 AA.
AC	Q9G176;				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Poliiovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1).				
DE	PVR1L OR PVR1 OR HVEC.				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.				
OX	NCBI_TaxId=9823;				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=21176378; PubMed=11277703;				
RX	Maline R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J., Cohen G.H.,				
RA	"Porcine HvEC, a member of the highly conserved HvEC/nectin 1 family, is a functional alphaherpesvirus receptor."				
RT	Virology 28:315-328(2001).				
RL	-1- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.				
CC	-1- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.				
CC	-1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.				
CC	-1- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	EMBL: AF308632; AAC30281.1;				
DR	HSSP; P06907; INEV.				
DR	InterPro; IPR007110; IG-1-like.				
DR	InterPro; IPR003596; IG_V.				
DR	Pfam; PF00447; Ig_2.				
DR	SMART; SM00406; IGV_1.				
DR	PROSITE; PS50835; IG-LIKE; 2.				
KW	Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane; Repeat; Glycoprotein; Signal.				
FT	SIGNAL	1	30		POTENTIAL.
FT	CHAIN	31	515		POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
FT	DOMAIN	31	355		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	356	376		POTENTIAL.
FT	DOMAIN	377	515		CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	31	141		IG-LIKE V-TYPE.
FT	DOMAIN	145	243		IG-LIKE C2-TYPE 1.
FT	DOMAIN	247	334		IG-LIKE C2-TYPE 2.
FT	DOMAIN	437	443		POLY-GLU.

FT DOMAIN 444 447 POLY-GLY.
 FT DISULFID 51 124 BY SIMILARITY.
 FT DISULFID 172 226 BY SIMILARITY.
 FT DISULFID 269 316 BY SIMILARITY.
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 515 AA, 57047 MW, BPAB00320DEJ785 CRC64;

Query Match 11.8%; Score 259.5; DB 1; Length 515;
 Best Local Similarity 24.5%; Pred. No. 2.2e-11;
 Matches 107; Conservative 61; Mismatches 165; Indels 103; Gaps 18;

QY 34 VVYIEGAVATISGVKSDSVQQLNPNKQITFRDPFLKDSFQLNFSSEKVL 93
 DB 62 ITQVWQKATNGSKON-----VAINPMAGVAVLAPYR-----ERVEFLRPSTDOTIRL 111
 QY 94 TNVSIIDEGRYFCQLYTDP--QESYTTITVIVPNNLMIDQ-----KDTAVEGEE 143
 DB 112 SRLLEDEGVYICFATFPAGNRESQNLITVMKPTWIEGTQAVLRAKKGDKV---- 167
 QY 144 IENVCTMAKRPATITWFKNKEIKGKSEVEE---SDVYVTSQMLKVKHEDGVV 200
 DB 168 LVATCTBANGKPPVSW---ETHLKGAEVYQIRPNNGVIVISRYLVPSEDEKQSL 224
 QY 201 ICQVHPAVTGNLTQRY-----LEVQKPOVHIQ--MTYPLQGLTREGDAFELTCEAI 252
 DB 225 ACIV-----NHYMDRFRESLTLNVQYEPVITIEGDGWLQRM-----VKLTCKAD 272
 QY 253 GKPOVAVTVYRVDENPQNAVLSGPNLFIN--LNKTDNTYCEASNTVKGKHSYMLX 311
 DB 273 ANPATEYHTWTLNGSLPKVEAQNRLTFRGPTNEMAGTYCEANPTGTRSGOVEN 332
 QY 312 VYDPTTIPPTTTTITTTTITTTTITTTITTSRAGEEG--TIGADVAVIGVVA---VVV 367
 DB 333 ITPEPTPSP-----HGRAGVYPAIIGGVGSLVLV 368
 QY 368 PAMLCILITIGRYARKHYFT-----HEAKGA-----DMAADADR 405
 DB 369 FVVGIVVALCRHRHTKGYSTKSHVYNGNGSKAGIPQHPMAQLQYFEDSDDEKA 428
 QY 406 IINAGGNGSEKKE 421
 DB 429 --GPLGGSSYESEEE 442

RESULT 2

ID_PVR1_HUMAN STANDARD; PRT; 517 AA.
 AC Q15223; Q15465; Q9HBE6; Q9HBM2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (Hvrc) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR) (CD111 antigen).
 GN PVR1 OR PVR1 OR HVRC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=95237621; PubMed=7721102;
 RA Lopez M., Eberle F., Mactel M.-G., Gabert J., Barin F., Maro C., Dubreuil P.;
 RT "cDNA characterization and chromosomal localization of a gene related to the poliovirus receptor gene";

RL Gene 155:261-265 (1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=98279152; PubMed=9616127;
 RA Geraghty R.J., Krummenacher G., Cohen G.H., Eisenberg R.J., Spear P.G.;
 RT "Entry of alphaherpesviruses mediated by poliovirus receptor-related protein 1 and poliovirus receptor";
 RL Science 280:1618-1620 (1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
 RX MEDLINE=21256041; PubMed=11356977;
 RA Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J., Campadelli-Fiume G., Dubreuil P.;
 RT "Novel, soluble isoform of the herpes simplex virus (HSV) receptor nectin (or pvr1-Hvrc) modulates positively and negatively susceptibility to HSV infection";
 RL J. Virol. 75:5684-5691 (2001).
 RN [4]
 RP SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE. MEDLINE=20392396; PubMed=10932188;
 RX Suzuki K., Hu D., Bustos T., Zlotogora J., Richiari-Costa A., Helms J.A., Spritz R.A.;
 RA "Mutations of PVR1, encoding a cell-cell adhesion molecule/herpesvirus receptor, in cleft lip/palate-ectodermal dysplasia";
 RT Nat. Genet. 25:427-430 (2000).
 RL - FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
 CC - SUBUNIT: Interacts with HSV glycoprotein D (gD).
 CC - SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and delta). Secreted (isoform gamma).
 CC - ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=Delta;
 CC IsoId=Q15223-1; Sequence=Displayed;
 CC Name=Alpha;
 CC IsoId=Q15223-2; Sequence=VSP_002626, VSP_002627;
 CC Name=Gamma;
 CC IsoId=Q15223-3; Sequence=VSP_002624, VSP_002625;
 CC - DISEASE: Defects in PVR1 are a cause of cleft lip/palate-ectodermal dysplasia syndrome (CLPED1) [MIM:225000]. CLPED1 is responsible for allelic forms known as Margarita island ectodermal dysplasia [MIM:225060] and Zlotogora-Oguz syndrome.
 CC - SIMILARITY: Contains 2 immunoglobulin-like V-type domain.
 CC - SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC - DATABASE: NAME=PROV; NOTE=PROV 2:45-49 (2001);
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/200569330_g.htm".
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb.ch/announce/> or send an email to license@isb.ch).
 CC
 DR EMBL: X76400; CAA53980.2; ALT_INIT.
 DR EMBL: AF060231; AAC23798.1; -
 DR EMBL: AY029539; AAK3124.1; -
 DR EMBL: AF252867; AAG16648.1; -
 DR EMBL: AF196768; AAG16648.1; JOINED.
 DR EMBL: AF196769; AAG16648.1; JOINED.
 DR EMBL: AF196770; AAG16648.1; JOINED.
 DR EMBL: AF196771; AAG16648.1; JOINED.
 DR EMBL: AF196774; AAG16649.1; -
 DR EMBL: AF196768; AAG16649.1; JOINED.
 DR EMBL: AF196769; AAG16649.1; JOINED.
 DR EMBL: AF196770; AAG16649.1; JOINED.
 DR EMBL: AF196771; AAG16649.1; JOINED.
 DR EMBL: AF196772; AAG16649.1; JOINED.
 DR EMBL: AF196773; AAG16649.1; JOINED.

DR Genew; HGNC:9706; PVR1.
 DR MIM; 60644; -.
 DR MIM; 22500; -.
 DR MIM; 22500; -.
 DR GO; GO:0016021; C.integral to membrane; NAS.
 DR GO; GO:004895; F.cel adhesion receptor activity; NAS.
 DR GO; GO:0015028; F.cel adhesion receptor activity; NAS.
 DR GO; GO:0006955; P.immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; Ig_Like; 2.
 DR Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
 Repeat; Glycoprotein; Signal; Alternative splicing.
 FT SIGNAL 1 30
 FT CHAIN 31 517
 FT DOMAIN 31 355
 FT TRANSMEM 356 376
 FT DOMAIN 377 517
 FT DOMAIN 31 141
 FT DOMAIN 149 238
 FT DOMAIN 247 334
 FT DOMAIN 437 444
 FT DOMAIN 445 449
 FT DISULFID 51 124
 FT DISULFID 172 226
 FT DISULFID 269 316
 FT CARBOHYD 36 72
 FT CARBOHYD 72 72
 FT CARBOHYD 139 139
 FT CARBOHYD 202 202
 FT CARBOHYD 286 286
 FT CARBOHYD 297 297
 FT CARBOHYD 307 307
 FT CARBOHYD 332 332
 FT VASPLIC 335 352
 FT VASPLIC 353 517
 FT VASPLIC 336 458
 FT VASPLIC 459 517
 FT SEQUENCE 517 AA; 57158 MW; DF34C8AE8C93BE6D CRC64;
 Query Match 11.5%; Score 252.5; DB 1; Length 517;
 Best local similarity 25.2%; Pred. No. 7e-11;
 Matches 104; Conservative 59; Mismatches 155; Indels 95; Gaps 19;
 QY 56 IQLNPNRQITVYFDFRLKDSRFOLNFSSELKSLINVSISDERYFCQLTDP-- 113
 DB 78 VAINPMSGVSLAPYR---ERVEFLRPSTDTGILSRLELDEGVYICERPTPTGN 133
 QY 114 QESTTITVLPSPNNLMIDIKD-TAVGESEIEV--NCTAMASKPATITRMFGKNEK 169
 DB 134 RESQINLVAKPTNWIEGTQAVLRKKGDQDKLVATCTISANGKPPSVSM--ETRLK 190
 QY 170 GKSEVEEK--SDMYTYSQMLKVKHKEDGVPIQVCHPAVGNQIQRY-----LEV 221
 DB 191 GEAEVQELRNNGVYTVISRYLVPSSRAHQSLACTV-----NTHDRFKESLTNV 243
 QY 222 QYKQVHIO--MTYPIQGLTRFEDAFELTGEALGKQPVWTVVVRVDEMPQHAVLSGP 278
 DB 244 QYEEVLTIEGPDGMVYIQMD-----VLTICKADANPAPAYHNTTLNGSLPKGVKQRN 298

QY 279 NLFINN-LNKDNGTYRCEASNIYGAHSDYMLVYDPTTPTTTTITTTTTITL 337
 DB 299 TLFPKGINSLAGTYICATNPISGRSGVEVNTFPPTSP----- 343
 QY 338 TITDSPAAGEG-TIGADVAVIGYVAVVFMCLLITLGRYFA---RH--KGYFT 390
 DB 344 -----EHGRAGVPTPAIGVAGSI---LVLIVVGIVLALRRRHFTKGDYST 391
 QY 391 -----HEAKGA-----DPAADADTAIINABGQNNSEKKE 421
 DB 392 KKAHYNGYSKAGIPQHHPMAQNLQYPPDSDEKKA--GPLGSSSYEEEEE 442
 RESULT 3
 ID PVR2 MOUSE STANDARD; PRT; 530 AA.
 AC P32507; 062096;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Poliovirus receptor related protein 2 precursor (Murine herpesvirus
 entry protein B) (HvB) (Nectin 2) (poliovirus receptor homolog).
 GN PVR2 OR PVS OR PVR OR MPH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=92219365; PubMed=1560525;
 RA Morrison M.E., Racanelli V.R.;
 RT "Molecular cloning and expression of a murine homolog of the human
 poliovirus receptor gene.";
 RL J. Virol. 66:2807-2813 (1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RX STRAIN=C57BL/6; TISSUE=Brain;
 MEDLINE=94179228; PubMed=8132569;
 RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
 RT "Amino acid residues on human poliovirus receptor involved in
 interaction with poliovirus.";
 RL J. Biol. Chem. 269:8431-8438 (1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RX STRAIN=FVB/N; TISSUE=Colon;
 MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.U., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millhys S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Vallion D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
 RA Rahy J., Helton E., Kettelman M., Madan A., Rodighiero S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shachenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=99214397; PubMed=10196354;
 RA Shukla D., Rowe C.L., Dong Y., Racanelli V.R., Spear P.G.;
 RT "The murine homolog (Mpr) of human herpesvirus entry protein B (HvB)
 mediates entry of pseudotyped virus but not herpes simplex virus
 types 1 and 2.";

FT	CARBOHYD	137	137	N-LINKED (GLCNAC...)	(POTENTIAL).
FT	CARBOHYD	324	324	N-LINKED (GLCNAC...)	(POTENTIAL).
FT	VARSPLIC	351	479	NTAAGGATGGIIGGTAATATATAATGILICROQRKSGCTL	
FT				.GAEBDEDLBGPSTYPTPRAKLEAOQMPSQLFTLGASEH	
FT				SPLKTFFPDAGASCTEQEMPRYNHELPTLEERGSLHPAGTS	
FT				LGSPIF -> RASPRDVGPLWVAGVTLLVLLLAGSIA	
FT				FILIRVRRRRSPCGAGGADGGFYDPKPQVLNGSDPVF	
FT				MTPVVGPMSEDDGDKEEEREEBEKKKELMPPPALDDDM	
FT				ESOLDGSLISRRAYVV (in isoform Alpha).	
FT	VARSPLIC	480	538	/FTID=VSP_002628.	
FT				Missing (in isoform Alpha).	
FT				/FTID=VSP_002629.	
SO	SEQUENCE	538 AA;	57742 MW;	3AE4FE3E92FEF624 CRC64;	
<hr/>					
Query Match		10.9%;	Score 238.5;	DB 1;	Length 538;
Best Local Similarity		22.8%;	Pred. No. 7.6e-10;		
Matches 110;		Conservative 63;	Mismatches 196;	Indels 113;	Gaps 17
Oy		2	AAPGLRLRLLLLLLSAALLPTGDQQLFTDXDVIVIEEVANTISCQVKNKSDSVTQLNRP	61	
Db		12	SPRPFLMLPRLILLL-----LLETG-AQDYRVGVULREVRG-----QLGGTYELRCHLLRP	59	
Oy		62	-----NRQTIFRDPRPLKDSRF-----QLNNSSC-----	87	
Db		60	VPGLYISLVTWORPDAPRNQNV--AAFHPRMGSPFPSPKPSERLSFVSASKOSTGODTE	117	
Oy		88	----ELKXSLTNVISIDEGRYFCOLYDPR--PQESYTITIVLVPPRNIMIDIOKDTAVEG	141	
Db		118	AELQDATLALHGLVEDEGNATCEPAITPFKKSVAQMTRVIARPN-QAQAOKYTESOD	176	
Oy		142	EETVENCTAMASKPATITIPFKG-KNELKGSEVEWMSDMYTVTSQLMKVHKEDDGVPV	200	
Db		177	PTVALCISKRGEPRIISMUSLSDWEAKERQVSGTLAIVTVISRFLVPSGRADGVTV	236	
Oy		201	ICQVEHAVNTGNLTQSYLEVQYKPOVNIQMTYPLQGLTBREGDAPELTCEALIGKROPVMV	260	
Db		237	TCKTEHSHFEPRPALIPTLSIKRYPEVIS-GYDDNMVLTGRTD-TLSCDVRSNDPEPTY	294	
Oy		261	TWVEVDDEMPHOAVLASGPNLFINNINKTNDGTVCASNIVGKAHSDFMYLVYDPTTIP	320	
Db		295	DWSITSGTFPSAIVAQSOLIVHAVDLSLPTTFVCTVNNAVGMGRAEQVIVRETPNT--	352	
Oy		321	PERTTTTTTTTTTTILITLITDSAGESEGITGADVAVTGVAVVVFYAMLCLILLCRY	380	
Db		353	-----AGAGATGG-----IIIGLIAAIATAVMAATGILICR	383	
Oy		381	FARRHGTYFTHEAKGADAADAD-----TAINAE-----GGONNSEEKKE	421	
Db		384	QQREGEI-----LOGAEDEDLBGPSPYKPTPRPAKLEAOQMPSQLFTLGASEHSLKTP	438	
Oy		422	YF 423		
Db		439	YF 440		

RESULT 5
PVR_CERAE STANDARD; PRT; 417 AA.

AC P32506;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Poliovirus receptor precursor.
GN PVR OR PVS.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
NC NCB1_Taxid=9534;
LN [1]

RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).
RC TISSUE=Kidney;
RX MEDLINE=93059651; PubMed=1331508;

OY	57	QLNLNPR-----QTIVRDRRLPLKDSFPOLLNPSSELSKSLTVVS-----ISDEGRY	104
Db	62	SQLTWSHGSGSMANVHQTOGPNYSPPKLEFVAALGLTFLDASLRMGFLRPDEGNY	121
OY	105	FCQLYTDPPESEYTT--ITLVEPPRLMTIDIQDAVEGESELEV-NCTAMASKPATITR	160
Db	122	TC-LFTVTFPGSGRSVDLWLRVLAKPQV-TAEVCK-VQLTKKPVAVACVSGRGPRAHIT	178
OY	161	WFKGNKELKKGSEVEE-----WSDMYTTSQMLKVHEDDGVPVPCGVHEPAVYGNLQTO	216
Db	179	W--HSDLGGMNPNTSQAPGLSPGLSGTVTSLMILVPSQVDGKSTCKVHEHSFKPKOLLT	235
OY	217	RYLEVOYKPPVHIQMTPTLOGLTFEEDGPAFLTECAIGKPPVMTWVRVVDDEMQHVLVS	276
Db	236	VNLTVYPPPEVVIS-GVDNNWYLSQNEA-ILTCARASNPEPTGYNTWSTMGLPLPFAVAQ	293
OY	277	GENLFINNLKNTDNGTYRCESASNVGCAHSDYMLVYVDPPTTPTPTTTTTTTTTTTTI	336
Db	294	GAQQLILPPVVKPIITTFICIVNTALGARQAEILTVQVEKGPSEPS-----	338
OY	337	LTITTSRAGEBGTIGADVHIGVAVVAFMLCLILIGRYFARHKGH----YFTHE	392
Db	339	-----GSSNIITILLIGIVI---LTLILLIGVYFYHSRCGRFLMCHHL	380
OY	393	AKGADDAADADTALINAEQGNNSSEKKE	421
Db	381	SPSSEHNSA-----SANGYISYSDVSR	404

RESULT 6

FPRL MOUSE	ID	FPRL MOUSE	STANDARD	PRT	515 AA.
AC	Q9UKF6; Q9ERL5; Q9Q117;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Poliiovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1).				
DE	FPRL1 OR PRL1 OR HVEC.				
GN	Mus musculus (Mouse).				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
CC	NCBI_TaxId=10090;				
CX	[1]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=20243787; PubMed=10781093;				
RX	Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J., Lecocq E., Dubrenil P., Campadelli-Fume G.;				
RA	"The murine homolog of human nectin delta serves as a species nonspecific mediator for entry of human and animal alpha herpesviruses in a pathway independent of detectable binding to gD."				
RT	Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).				
RL	[2]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=20541977; PubMed=11090177;				
RX	Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;				
RA	"Striking similarity of murine nectin-1alpha to human nectin-1alpha (HvEC) in sequence and activity as a glycoprotein D receptor for alphaherpesvirus entry."				
RT	J. Virol. 74:11773-11781(2000).				
RL	[3]				
RN	SEQUENCE FROM N.A.				
RP	STRAIN=Swiss Webster;				
RA	Zhan J., Wimmer E.;				
RT	"Mouse nectin-1 (mPRL1), a herpesvirus receptor, is expressed in the floor plate during embryogenesis, suggesting a role in neural development."				
RL	Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.				
CC	-1- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.				
CC	-1- SUBUNIT: Interacts with HSV glycoprotein D (gD).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				


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FT      CONFLICT      75      75      (Potential).
FT      CONFLICT      92      S -> G (IN REF. 1).
FT      CONFLICT      119     T -> I (IN REF. 1).
FT      CONFLICT      187     E -> Q (IN REF. 1).
FT      CONFLICT      213     R -> P (IN REF. 1).
FT      CONFLICT      225     I -> F (IN REF. 1).
SQ      SEQUENCE      344 AA; 37984 MW; C885B8A52C148554 C8C64;

Query Match      10.6%; Score 232; DB 1; Length 344;
Best Local Similarity 26.2%; Pred. No. 1.3e-09;
Matches      85; Conservative 57; Mismatches 133; Indels 50; Gaps 15;

QY      10 LLLLLLAAALIFPTG---DGNLFTK---DYVIEGAVATISCCVKNKSDSVIQLNPN 62
DB      14 LVVSLRLFLFPTGTVPVRSADATFPKXMDVTVVAGSASATLRCIT---DKRVTVVWLN 70
QY      63 RQTI-YFRDPRPLKDSRFQNLNFSSELKSLTNVNSISDEGRYFQQLYTD--PROESYTTI 120
DB      71 RSTIIYAGNDKMKCDLPRVVLSTNTQYSEIQNVVDVDEGRPYTCVTDNHPKTSRVHL 130
QY      121 TVLVPNNMTIDIQDQYAV-EGEIEVNTCTAMASXPATTIRFKGNKELKGSSEVEWSD 179
DB      131 IVQVSPK--IVEISSDISINEGNNSITLCIA-TGRPEPTVWRIHSPKAVGVSEDEYLE 187
QY      180 MYVTSLMLKYNH---KEDDGVPIQCVHEHRAVGNLQTVYLVQYKPYQHIQMTPLQ 236
DB      188 IQGITREOSGEYECASNDVAAPVRRVK-----VTVPYPTIS---EAK 229
QY      237 GL-TREGDAFELTCEAIKPPQVWTVVTVVVDDEMPQ-----HAVISGNPLFINLN 286
DB      230 GTGVFVGQKGLQCEASAVPS-ABEQWFKDKRLVEGKKGKGVENRPLSLTLTF--NVS 286
QY      287 KTDNCTYCEASNTYGAHSDYMLY 311
DB      287 EHDYGNVTCVASNKLGHNTNASIMLF 311

RESULT 9
PVR_HUMAN
ID      PVR_HUMAN      STANDARD.      PRT;      417 AA.
AC      P15151; P15152; Q15267; Q15268;
DT      01-APR-1990 (Rel. 14, Created)
DI      01-FEB-1996 (Rel. 33, Last sequence update)
DE      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Poliovirus receptor precursor (CD155 antigen).
GN      PVR OR PVS.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. PubMed=2538245;
RX      Mendelsohn C.L., Wimmer E., Racanelli V.R.;
RA      "Cellular receptor for poliovirus: molecular cloning, nucleotide
RT      sequence, and expression of a new member of the immunoglobulin
RT      superfamily.";
RL      Cell 56:855-865 (1989).
RN      [2]
RP      REVISIONS.
RA      Racanelli V.R.;
RL      Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RX      MEDLINE=9106015; PubMed=2170108;
RA      Koike S., Horie H., Ise I., Okitsu A., Yoshida M., Iizuka N.,
RA      Takeuchi K., Takegami T., Nomoto A.;
RT      "The poliovirus receptor protein is produced both as membrane-bound
RT      and secreted forms.";
RL      EMBO J. 9:3217-3224 (1990).
RN      [4]
RP      SEQUENCE FROM N.A.

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RA      Kodoyianni V., Severin J., Ge Y., Grable J., Kvistad E., Gordon J.,
RA      Shannon M., Brower A., Olsen A.S., Smith L.M.;
RT      "Sequence analysis of a 1Mb region in 19q13.2 containing a zinc finger
RT      gene cluster.";
RL      Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      DOMAINS.
RX      MEDLINE=91239515; PubMed=1851992;
RA      Koike S., Ise I., Nomoto A.;
RT      "Functional domains of the poliovirus receptor";
RL      Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108 (1991).
RN      [6]
RP      NUCLEOTIDE SEQUENCE OF CARBOHYDRATE-LINKAGE SITES.
RX      MEDLINE=93059689; PubMed=1331527;
RA      Zibert A., Wimmer E.;
RT      "N-glycosylation of the virus binding domain is not essential for
RT      function of the human poliovirus receptor.";
RL      J. Virol. 66:7368-7373 (1992).
CC      -1- FUNCTION: Not known. Used by poliovirus to bind and enter the
CC      cell.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
CC      delta). Secreted (isoforms beta and gamma).
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=4;
CC      Name=Alpha;
CC      IsoId=P15151-1; Sequence=Displayed;
CC      Name=Beta;
CC      IsoId=P15151-2; Sequence=VSP_002617;
CC      Name=Gamma;
CC      IsoId=P15151-3; Sequence=VSP_002618, VSP_002619;
CC      Name=Delta;
CC      IsoId=P15151-4; Sequence=VSP_002620, VSP_002621;
CC      -1- MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR
CC      VIRUS BINDING AND UPTAKE.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC      -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC      -1- DATABASES: NAME=PROV; NOTE=CD guide CD155 entry;
CC      WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb.slb.ch).
CC      -----
DR      EMBL; M24407; AAA36461.1; -
DR      EMBL; M24406; AAA36462.1; -
DR      EMBL; X64116; CAA45478.1; -
DR      EMBL; X64117; CAA45478.1; JOINED
DR      EMBL; X64118; CAA45478.1; JOINED
DR      EMBL; X64119; CAA45478.1; JOINED
DR      EMBL; X64120; CAA45478.1; JOINED
DR      EMBL; X64121; CAA45478.1; JOINED
DR      EMBL; X64122; CAA45478.1; JOINED
DR      EMBL; X64123; CAA45478.1; JOINED
DR      EMBL; X64115; CAA45479.1; -
DR      EMBL; X64117; CAA45479.1; JOINED
DR      EMBL; X64118; CAA45479.1; JOINED
DR      EMBL; X64119; CAA45479.1; JOINED
DR      EMBL; X64120; CAA45479.1; JOINED
DR      EMBL; X64121; CAA45479.1; JOINED
DR      EMBL; X64122; CAA45479.1; JOINED
DR      EMBL; X64123; CAA45479.1; JOINED
DR      EMBL; X64116; CAA45480.1; -
DR      EMBL; X64117; CAA45480.1; JOINED
DR      EMBL; X64118; CAA45480.1; JOINED
DR      EMBL; X64119; CAA45480.1; JOINED
DR      EMBL; X64120; CAA45480.1; JOINED
DR      EMBL; X64121; CAA45480.1; JOINED
DR      EMBL; X64122; CAA45480.1; JOINED
DR      EMBL; X64123; CAA45480.1; JOINED
DR      EMBL; AC068848; AAF59803.1; -

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DR PIR; A43024; RMHUPD.
DR PIR; S12048; RMHUPA.
DR Genew; HGNC:9705; PVR.
DR MIM; 173850; -.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007125; P:invasive growth; TAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; Ig_Like; 3.
KW Immunoglobulin domain; Receptor; Polymorphism.
KW Repeat; Antigen; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 417
FT DOMAIN 21 343
FT TRANSMEM 344 367
FT DOMAIN 368 417
FT DOMAIN 24 139
FT DOMAIN 145 237
FT DOMAIN 244 328
FT DISULFID 49 123
FT DISULFID 166 221
FT DISULFID 266 312
FT CARBOHYD 105 105
FT CARBOHYD 120 120
FT CARBOHYD 188 188
FT CARBOHYD 218 218
FT CARBOHYD 237 237
FT CARBOHYD 278 278
FT CARBOHYD 307 307
FT CARBOHYD 313 313
FT VASPLIC 340 340
FT VASPLIC 331 331
FT VASPLIC 332 332
FT VASPLIC 385 392
FT VASPLIC 393 417
FT VASPLIC 67 67
FT VARIANT 340 340
FT SEQUENCE 417 AA; 45302 MW; DISC012CE85169B CRC64;

Query Match 10.5%; Score 231.5; DB 1; Length 417;
Best Local Similarity 25.3%; Pred. No. 1.8e-09;
Matches 101; Conservative 53; Mismatches 174; Indels 71; Gaps 16;

10 LLLLLLAAALIPFGDGNLFKQVTV-----IGEVATISQV---NKSDDSYIQL 58
11 LLLVALVLVSWPSPGTG-----DVVQAPRVGFLGDSVTLPCYQLQVNMETVHSQL 64
59 L-----NPNRQITVPDRPLKDRFOLLNFSSELTXTSLTNVS-----ISDEGRYFCQ 167
65 TWAHGESGSMVAHVHQIQGSPYSSEKLEFVAALGAEIRNASIRMGRLAVEBEGNYTC- 123
108 LYTDPQDSYTT---ITVLVPPRNIMIDIQKTAVEGESELEV-NCTAMASKPATTRWEK 163
124 LFTVFPQGSRSVDIMRLVLAQPN-TAEVQR-VQLTGEFVPMARCVSTGCRPPAQLTWSH 181
164 GNMKLKGSVEEEM-SDMYTTSQMLKMHKEDGVAVICQVEHPATGNLQGRYIEVQ 222
182 DLGGPNTSQVPGSLSGVTYVTSMLVPSQVDGKAVTCVNEHSEKQQLITLVNLTIV 241
223 YKPOVHQMTPLOGLTREGDAFELTCEALGKPPVWVWTVRVYDDEMPQHAVLSGPNLFI 282

DB 242 YPPEVSIS-GYDNNMYLQONEA-TLTCDAKSNPEPTGYNNSTMGPLPPRAVAGAOQLI 299
QY 283 NMLKNTDNGTYRCASNVIGKAHSDYMLVYDPEPTIIPPTTTTTTTTTTTTTTTTT 342
DB 300 RVPDKPINTLLICNVNTNLGARQAEFLTVQVKE-----GPPSEHS----- 338
QY 343 SRAGEGTIGAVDHAIVGVAVVVFAPMLCLIIILGSYF 381
DB 339 -----GSRNALITVLGILVF--LTLIGLITF 365

RESULT 10
NRI RAT STANDARD; PRT; 344 AA.
ID NRI RAT
AC Q62718;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurotrophin precursor (GP65).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 217-229.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=95198094; PubMed=7891157;
RA Salzer A.F., Canoll P.D., Wolfgang M.J., Rosen C.L., D'Eustachio P.,
RA Salzer J.L.;
RT "Cloning of neurotrophin defines a new subfamily of differentially
RT expressed neural cell adhesion molecules.";
RL J. Neurosci. 15:2141-2156(1995).
CC - FUNCTION: Neural cell adhesion molecule.
CC - SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC - TISSUE SPECIFICITY: Central nervous system.
CC - DEVELOPMENTAL STAGE: Expressed at high levels in several
CC developing projection systems: in neurons of the thalamus,
CC subplate, and lower cortical laminae in the forebrain and in the
CC pontine nucleus, cerebellar granule cells, and Purkinje cells in
CC the hindbrain.
CC - SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
CC family.
CC - SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; U16845; AAA67445.1; -.
CC PIR; I56551; I56551.
CC InterPro: IPR007110; IG-like.
CC InterPro: IPR003598; IG_c2.
CC SMART; SM00408; IGc2; 2.
CC PROSITE; PS50835; IG_Like; 3.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal; Lipoprotein.
FT SIGNAL 1 31
FT CHAIN 32 321
FT PROPEP 322 344
FT DOMAIN 39 326
FT DOMAIN 136 218
FT DOMAIN 222 309
FT DOMAIN 57 115
FT DISULFID 157 201
FT DISULFID 243 295
FT CARBOHYD 44 44
FT CARBOHYD 70 70
FT CARBOHYD 152 152
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT LIPID 321 321 GPI-anchor amidated asparagine (Potential).

SEQUENCE 344 AA; 37998 MW; CBB39BE5B3B224 CRC64;
 Query Match 10.5%; Score 231; DB 1; Length 344;
 Best Local Similarity 26.2%; Pred. No. 1.5e-09;
 Matches 85; Conservative 56; Mismatches 134; Indels 50; Gaps 15;

QY LLLLLLSAALIPFG---DQGNLFK---DVTVEGEVATISCOVNSDSDVQLNPN 62
 DB LVVVSLRLFLVFTGVPVPSGDAITPKAMDVTYRQGSATLRCTI---DNRTVRYAWLN 70
 QY RGTI-YRDPFRPKDSRFQOLNFSSELKVS/LTNVISISDEGRYFCQLYTD-PPQSYTTI 120
 DB RSTILYAGNDKWCCLDPVLLSNQTQYSIEIQNVVDYDEGPYCSVQTDNHPKTSRVHL 130
 QY TLVPRRLMIDIQDITAV-EGEEIEVNTAMASKPATIIRFKNKELKGSVEEMSD 179
 DB IVQVSPK--IVBISDISINGNISLTCTIA-TGRPEPTVWRHISPAVGFVSEDEYLE 187
 QY MYTVTSQMLKXVH---KEDGVVPIQVYEHPAVTGNLTQRYLEVOYKPOVHIQMTYPLQ 236
 DB IGGITREQSGEGYECASNDVAAPVRYRN-----VYVNPPIYIS-----EAK 229
 QY 237 GL-TREGDAFELTCEAIKGPQVWMTYRVVDEMPQ-----HAVLSGPNLFINNLN 286
 DB GTGVVPGQKGTLCQCEASAVPS-AEFQWKDKRLVEGKGVKVENRPFSLTFE--NVS 286
 QY 287 KTDNGYRCEASNIVGKAHSDYMLY 311
 DB EHDYGNVTCVASNKLGHNTASIMLF 311

RESULT 11

ID NTRI HUMAN STANDARD; PRT; 344 AA.

AC 09P121;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Neurotrophin precursor (hnt).

GN NT.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCB1_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Li G., Jin J., Tan X., Yuan J., Qiang B.

RT "Cloning and identification of human neurotrophin full length cDNA."

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Neural cell adhesion molecule.

CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. Ig1ON family.

CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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CC or send an email to license@isb-sib.ch).

CC EMBL; AF126426; AAF7591.1; -

DR MM; 607938; -

DR GO; GO:0008038; P:neural cell recognition; TAS.

DR GO; GO:0008038; P:neural cell recognition; TAS.

DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_c2.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00408; IgC2; 2.
 DR PROSITE; PSS0835; IG_Like; 3.
 KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
 KW Repeat; Signal; Lipoprotein.

FT SIGNAL 1 31
 FT CHAIN 32 321
 FT PROPEP 322 344
 FT DOMAIN 39 126
 FT DOMAIN 136 218
 FT DOMAIN 222 309
 FT DISULFID 57 115
 FT DISULFID 157 201
 FT DISULFID 243 295
 FT CARBOHYD 44 44
 FT CARBOHYD 70 70
 FT CARBOHYD 152 152
 FT CARBOHYD 284 284
 FT CARBOHYD 292 292
 FT CARBOHYD 305 305
 FT CARBOHYD 321 321
 FT LIPID 321 321

SEQUENCE 344 AA; 37971 MW; DA4D12C295ABBE3A CRC64;
 Query Match 10.4%; Score 229; DB 1; Length 344;
 Best Local Similarity 26.3%; Pred. No. 2.1e-09;
 Matches 85; Conservative 57; Mismatches 135; Indels 46; Gaps 15;

QY LLLLLLSAALIPFG---DQGNLFK---DVTVEGEVATISCOVNSDSDVQLNPN 62
 DB LVVVSLRLFLVFTGVPVPSGDAITPKAMDVTYRQGSATLRCTI---DNRTVRYAWLN 70
 QY RGTI-YRDPFRPKDSRFQOLNFSSELKVS/LTNVISISDEGRYFCQLYTD-PPQSYTTI 120
 DB RSTILYAGNDKWCCLDPVLLSNQTQYSIEIQNVVDYDEGPYCSVQTDNHPKTSRVHL 130
 QY TLVPRRLMIDIQDITAV-EGEEIEVNTAMASKPATIIRFKNKELKGSVEEMSD 179
 DB IVQVSPK--IVBISDISINGNISLTCTIA-TGRPEPTVWRHISPAVGFVSEDEYLE 187
 QY MYTVTSQMLKXVH---KEDGVVPIQVYEHPAVTGNLTQRYLEVOYKPOVHIQMTYPLQ 236
 DB IGGITREQSGEGYECASNDVAAPVRYRN-----VYVNPPIYIS-----EAK 229
 QY 237 GL-TREGDAFELTCEAIKGPQVWMTYRVVDEMPQ-----HAVLSGPNLFINNLN 286
 DB GTGVVPGQKGTLCQCEASAVPS-AEFQWKDKRLVEGKGVKVENRPFSLTFE--NVS 286
 QY 289 DNGYRCEASNIVGKAHSDYMLY 311
 DB DYGNTVTCVASNKLGHNTASIMLF 311

RESULT 12

ID NCM2 MOUSE STANDARD; PRT; 837 AA.

AC 035136; O35962;

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell

adhesion molecule) (R4B12).

GN NCM2 OR OCAM OR RNCAM.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCB1_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).

RC STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium;

[illegible]

```

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed most strongly in adult and fetal
CC brain.
CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U75330; AAB80803.1; -.
CC Genbank: H62040; NCAM2.
CC MIM: 602040; -.
DR GO: GO:0016021; C: integral to membrane, TAS.
DR GO: GO:0005886; C: plasma membrane, TAS.
DR GO: GO:0007158; P: neuronal cell adhesion, TAS.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00047; ig; 5.
DR SMART: SM00060; FN3; 2.
DR SMART: SM00408; IG_c2; 5.
DR PROSITE: PS50835; IG_LIKE; 5.
KW Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 19
FT CHAIN 20 837
FT DOMAIN 20 697 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 698 718
FT DOMAIN 719 837 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 837 837
FT DOMAIN 113 108 IG-LIKE C2-TYPE 1.
FT DOMAIN 113 202 IG-LIKE C2-TYPE 2.
FT DOMAIN 208 297 IG-LIKE C2-TYPE 3.
FT DOMAIN 302 396 IG-LIKE C2-TYPE 4.
FT DOMAIN 401 491 IG-LIKE C2-TYPE 5.
FT DOMAIN 482 581 FIBRONECTIN TYPE-III 1.
FT DOMAIN 594 678 FIBRONECTIN TYPE-III 2.
FT DISULFID 42 93 PROBABLE.
FT DISULFID 136 186 PROBABLE.
FT DISULFID 232 281 PROBABLE.
FT DISULFID 322 380 PROBABLE.
FT DISULFID 422 475 PROBABLE.
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 474 474 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 837 AA; 92932 MW; CSD034106C5741C1 CRC64;

Query Match 10.1%; Score 222; DB 1; Length 837;
Best Local Similarity 23.3%; Pred. No. 2,1e-08;
Matches 115; Conservative 67; Mismatches 180; Indels 132; Gaps 24;

31 TKDVTI-----EGEVATISCOVKKSDSVIQLNPRQITVPRDF 71
102 TQETVLEITQKLTFRVSPQERKQGEDEAVICRVSAPAVSMULYNEEV----- 155
72 RPLKDSRFLINPSSSELKSLVNVSLSDSGRYFCQLYTDPQR-SYTTITVT--VPPRN 128
156 TTISDNRNLAFL-----ANNNLQILINIKSDEGIYCEGVEARGEIDPRDIIVNVPPAI 211
129 LMIDIGKD---TAVGESELEVNCTAMASKPATITRMFKGNELKQKSEVEWMSMTYV-- 183
212 SM--FQKSPNATAEKGSEMTSFCRASGS-PPPAISWFRNGKLT-----ENRKYTLKG 261

```

DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; IG_c2.
 DR Pfam: PF00047; fn3, 2.
 DR Pfam: PF00047; Ig, 5.
 DR SMART: SM00060; FN3, 2.
 DR SMART: SM00408; IGC2, 4.
 DR PROSITE: PS50835; IG_LIKE; 5.
 DR Cell adhesion: Glycoprotein; Transmembrane; Repeat;
 KW Immunoglobulin domain; Alternative splicing; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 1092
 FT
 FT DOMAIN 20 705
 FT TRANSMEM 706 723
 FT DOMAIN 724 1092
 FT DOMAIN 113 202
 FT DOMAIN 208 295
 FT DOMAIN 303 397
 FT DOMAIN 400 489
 FT DOMAIN 512 589
 FT DOMAIN 618 686
 FT DOMAIN 149 153
 FT DOMAIN 158 162
 FT DISULFID 41 93
 FT DISULFID 136 186
 FT DISULFID 232 282
 FT DISULFID 323 379
 FT DISULFID 420 473
 FT CARBOHYD 82 82
 FT CARBOHYD 219 219
 FT CARBOHYD 310 310
 FT CARBOHYD 341 341
 FT CARBOHYD 417 417
 FT CARBOHYD 443 443
 FT CARBOHYD 472 472
 SQ SEQUENCE 1092 AA; 118062 MW; CD236E0E8B7AD1 CAC64;
 Query Match 10.1%; Score 222; DB 1; Length 1092;
 Best Local Similarity 23.9%; Pred. No. 2.9e-08;
 Matches 81; Conservative 68; Mismatches 150; Indels 40; Gaps 15;

QY 32 KDVVIVGEVATISC---QVTKS---DDSVIQLN-----NRRQTYPRDPRPKDGRFOL 81
 DB 199 KDIVIVVPEPLIDARQIRVATAMDESIVLSCDADGFPDPRIWIKKEPIEDGB-EK 257
 QY 82 LNFSSSELKVSILNVISIDSGRYFCQLYTPDPOESYTTITVLVPPNLMIDIQDTAVSG 141
 DB 258 ISFNEDEKSEMTIYVEKEDEDEAYSC-IANNQAGAEAIVLKYAKPKMTYVENKTTVEH 316
 QY 142 EELVNCCTAMSKRATIRMKKKEIKGKSEVEEMDMVTY-----SQLMKVHKED 195
 DB 317 DEITLTCEA-SGDPIPSITWRTRARNT---SSEKTLIDGHIVKDHIRMSALTIKOIQT 372
 QY 196 DGEVVICQVEHPAVTGNLQOTRYLEVOYKPOVHIQMTYPLQGLTRGDATELTCEAIGKE 255
 DB 373 DAGEYFVCAVNP-IGVDMQAM-YFEVOYAPKIR---GPVVVYTWEGNPNVICDVLAAH 426
 QY 256 QPVAVTVRWVDDEMPH-----AVLSGP---NLFNNLAKTIDNGITRCESNIVGAAHD 307
 DB 427 S-AAVSWFRDQQLPSSNFSNIKYNPTSSLEVNDSSNDGNCVAVNSIGHSSE 485
 QY 308 YMLVYDPEPTIPPTTT 346
 DB 486 FILVQADTPSS---PAIRKVEPYSYTWIVFDESDAIGG 521

RESULT 15
 NPHN MOUSE STANDARD; PRT; 1242 AA.
 AC Q9QZS7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Nephrit precursor (Renal glomerulus-specific cell adhesion receptor).
 GN NPHS1 OR NPHN
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. AND SUBCELLULAR LOCATION.
 RX MEDLINE=99436348; PubMed=10504499;
 RA Holman L.B., St John P.L., Kovari I.A., Verma R., Holtsoefer H.,
 RA Abrahamson D.R.;
 RA "Nephrit localizes to the slit pore of the glomerular epithelial
 RT cell."
 RT Kidney Int. 56:1481-1491(1999).
 RL [2]
 RP INTERACTION WITH CD2AP.
 RX MEDLINE=21590051; PubMed=11733379;
 RA Shih N.Y., Li J., Cotran R., Mundel P., Miner J.H., Shaw A.S.;
 RT "CD2AP localizes to the slit diaphragm and binds to nephrin via a
 RT novel C-terminal domain."
 RL Am. J. Pathol. 159:2303-2308(2001).
 RN [3]
 RP INTERACTION WITH CD2AP AND NPHS2.
 RX MEDLINE=21590460; PubMed=11733557;
 RA Schwarz K., Simons W., Reiser U., Saleem M.A., Paul C., Kriz W.,
 RA Shaw A.S., Holzman L.B., Mundel P.;
 RT "Podocin, a raft-associated component of the glomerular slit
 RT diaphragm, interacts with CD2AP and nephrin."
 RL J. Clin. Invest. 108:1621-1629(2001).
 CC -1- FUNCTION: Seems to play a role in the development or function of
 CC the kidney glomerular filtration barrier. May anchor the podocyte
 CC slit diaphragm to the actin cytoskeleton.
 CC -1- SUBUNIT: Interacts with podocin/NPHS2 and with CD2AP C-terminal
 CC domain.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential). Located
 CC at podocyte slit diaphragm between podocyte foot processes.
 CC -1- TISSUE SPECIFICITY: Expressed in kidney glomeruli.
 CC -1- PTM: Phosphorylated on tyrosine residues (by similarity).
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily.
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
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 CC
 CC EMBL, AF168466; AAF03368.1; -
 DR MGD, MGI:1859637; Nphs1.
 DR GO, GO:0005515; F:protein binding; IPI.
 DR GO, GO:0007254; P:JNK cascade; IDA.
 DR GO, GO:000165; P:MAPKK cascade; IDA.
 DR InterPro: IPR008957; FN_III-Like.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR007110; IG_Like.
 DR InterPro: IPR003598; IG_c2.
 DR Pfam: PF00047; fn3, 1.
 DR Pfam: PF00047; Ig, 8.
 DR SMART: SM00060; FN3, 1.
 DR SMART: SM00408; IGC2, 1.
 DR PROSITE: PS50835; IG_LIKE; 8.
 KW Cell adhesion; Transmembrane; Signal; Glycoprotein;
 KW Immunoglobulin domain; Repeat; Phosphorylation.
 FT SIGNAL 1 22
 FT CHAIN 23 1242
 FT DOMAIN 23 1064
 FT TRANSMEM 1065 1086
 FT DOMAIN 1087 1242
 FT DOMAIN 125 130


```
FT DOMAIN 135 233 IG-LIKE C2-TYPE 2.
FT DOMAIN 242 333 IG-LIKE C2-TYPE 3.
FT DOMAIN 340 434 IG-LIKE C2-TYPE 4.
FT DOMAIN 440 540 IG-LIKE C2-TYPE 5.
FT DOMAIN 544 635 IG-LIKE C2-TYPE 6.
FT DOMAIN 740 832 IG-LIKE C2-TYPE 7.
FT DOMAIN 838 939 IG-LIKE C2-TYPE 8.
FT DOMAIN 941 1025 FIBROECTIN TYPE-III.
FT DISULFID 53 111 POTENTIAL.
FT DISULFID 160 217 POTENTIAL.
FT DISULFID 265 317 POTENTIAL.
FT DISULFID 361 417 POTENTIAL.
FT DISULFID 465 528 POTENTIAL.
FT DISULFID 567 623 POTENTIAL.
FT DISULFID 761 816 POTENTIAL.
FT DISULFID 863 920 POTENTIAL.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 547 547 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 680 680 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 708 708 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 908 908 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1242 AA; 134890 MW; 02D82180BF145092 CRC64;
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Query Match 10.1%; Score 221; DB 1; Length 1242;

Best Local Similarity 22.7%; Pred. No. 4e-08; Mismatches 164; Indels 54; Gaps 16;

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QY 5 GLRLRLLLLSAALIPTEGDN-----LFTKDYVIEGEVATISCCVNSKSD 53
Db 4 GTTRASILL--AGMLTGTGAQSVPVTSAPRGFWALSENLTVEGSTIKLMGCV-RAPG 59
QY 54 SVIQ-----LLNPNRQITVFRDRPLKDSRFQULNFSSSEHLKSLTNVSI SDEGRYFCQ 107
Db 60 SVVQWAKDGLLLGNPKIPGFPRYSLEGDS-----AKGEFHLLIEACDLSDAEYECQ 112
QY 108 LYTP--PQ--ESYTTITVLPNNLMIDIOXD--TAVEGEIEVNCMTAMASKPATIR 160
Db 113 VGRBELGPELVSPRVIILSVLPKYLQITPRAGSTVTVWAGQEVVTCVSGAKRPADII 172
QY 161 WFKGNKEIKG-KSEVEKWD--MYTVSQMLKVHKEDDGVPIQVEHPAVTGNLQTOR 217
Db 173 FIQGRIVEDVSSSVNEGSEKELFFTEAEAVTPOSSDNGQLVCEGSPALATPIKASF 232
QY 218 YLEVOYKQVHIQMTYP--LQGLTRGDAPELTCEAIGKQPVNMTVWRVDDEN-----P 270
Db 233 TMTLILFPFGPPV-IDWPGINAGHVRAGENLELPCTIAGGNPAPATLQMLKNGKQVSIAMGT 291
QY 271 QHAVLSEGNLFINNLNKTNDGT-YRCEASNIIVGKAHSDYMLYYVDPPTIIPPTTT---- 325
Db 292 EHAQAVASHVLMVTRPEDHGARLSCQSYNSVSAETQERSITL--QVTFPPSAVTIIGS 348
QY 326 TTTTITTTTITLITITDSR 344
Db 349 TSGENKNVTLCCILKSR 367
```

Search completed: July 7, 2004, 06:03:55
Job time : 29.874 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 ; Search time 59.1711 Seconds

(without alignments)
2255.564 Million cell updates/sec

Title: US-10-622-237-4

Perfect score: 2197
Sequence: 1 AAPPGRLRLRLLLLSAAL.....TAIINAGGQNNSEKKEYF 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2197	100.0	445	11	Q8R4L1 mus musculus
2	2193	99.8	445	11	Q8R3T6 mus musculus
3	2176.5	99.1	445	11	Q8R3M8 mus musculus
4	2166	98.6	442	4	Q8B2P4 mus musculus
5	2027	92.3	417	11	Q7TND1 mus musculus
6	2020.5	92.0	443	4	Q8N2P4 mus musculus
7	1631	74.2	336	11	Q8DCE7 mus musculus
8	1631	74.2	336	11	Q8DCE7 mus musculus
9	1615	73.5	333	4	Q8B2P4 mus musculus
10	1546	70.4	295	11	Q8Z2H8 mus musculus
11	1513.5	68.9	306	11	Q8Z2H8 mus musculus
12	1493	68.0	295	11	Q8Z2H8 mus musculus
13	1404	63.9	289	11	Q8Z2H8 mus musculus
14	1380.5	62.8	278	11	Q8Z2H8 mus musculus
15	897	40.8	435	4	Q8N3J6 mus musculus
16	895	40.7	437	4	Q8I2P8 mus musculus

17	864	39.3	404	11	Q8BLO9 mus musculus
18	860	39.1	404	11	Q8BLO9 mus musculus
19	857	39.0	395	11	Q8B2P4 mus musculus
20	854	38.9	395	11	Q8B2P4 mus musculus
21	800	36.4	394	13	Q7ZXX1 xenopus lae
22	766.5	34.9	388	4	Q8N2P4 mus musculus
23	757.5	34.5	388	11	Q8N2P4 mus musculus
24	739.5	33.7	396	11	Q8N2P4 mus musculus
25	732.5	33.3	398	4	Q8N2P4 mus musculus
26	730.5	33.2	381	4	Q8Y4A4 mus musculus
27	715.5	32.6	432	4	Q8Y4A4 mus musculus
28	371.5	16.9	163	11	Q8Y4A4 mus musculus
29	362.5	16.5	163	4	Q8Y4A4 mus musculus
30	360.5	16.4	152	11	Q8Y4A4 mus musculus
31	337.5	15.4	549	11	Q8Y4A4 mus musculus
32	334.5	15.2	549	11	Q8Y4A4 mus musculus
33	325.5	14.8	549	4	Q8Y4A4 mus musculus
34	323.2	14.7	234	4	Q8Y4A4 mus musculus
35	303.5	13.8	438	11	Q8Y4A4 mus musculus
36	303.5	13.8	510	11	Q8Y4A4 mus musculus
37	283	12.9	439	13	Q8Y4A4 mus musculus
38	270	12.0	407	4	Q8Y4A4 mus musculus
39	263	12.0	1482	5	Q8Y4A4 mus musculus
40	261.5	11.9	5175	5	Q8Y4A4 mus musculus
41	261.5	11.9	5198	5	Q8Y4A4 mus musculus
42	248.5	11.3	624	11	Q8Y4A4 mus musculus
43	248.5	11.3	789	11	Q8Y4A4 mus musculus
44	247.5	11.3	467	11	Q8Y4A4 mus musculus
45	247.5	11.3	510	4	Q8Y4A4 mus musculus

ALIGNMENTS

RESULT 1
ID Q8R4L1 PRELIMINARY; PRT; 445 AA.
AC Q8R4L1; 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Tumor suppressor in lung cancer 1.
GN IGSP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=129/Svj.
RC Fukami T., Maruyama T., Murakami Y.,
RT "Identification of murine orthologue of the TSUC1 gene."
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF434663; AAL86736.1; -
DR MGD; MGI:1889272; IGSP4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
DR GO; GO:000515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003598; IG-C2.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PR00047; ig1.3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IG2; 1.
DR PROSITE; PS00835; IG-LIKE; 3.
KW Immunoglobulin domain.
SQ
SEQUENCE 445 AA; 48664 MW; CSD5A070DAF70E55 CRC64;
Query Match 100.0%; Score 2197; DB 11; Length 445;
Best Local Similarity 100.0%; Pred. No. 7.3e-178;

Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAPPGLRLRLRLRLRLRLSAAALIPFGDGNLFTKDVTVIEGEVATISCCVNSKSDSVIQLN 60
Db 22 AAPGLRLRLRLRLRLRLSAAALIPFGDGNLFTKDVTVIEGEVATISCCVNSKSDSVIQLN 81
QY 61 PNRCTIYFRDPRPKDSRFQQLNFSSELKVSILTVNISIDEGRYFCQLYTDPPQESYTTI 120
Db 82 PNRCTIYFRDPRPKDSRFQQLNFSSELKVSILTVNISIDEGRYFCQLYTDPPQESYTTI 141
QY 121 TVLPPRLMLDIOKOTAVEGEIEVNCCTAMASKPATITIRPFKNKELKXKSEVEEWSDM 180
Db 142 TVLPPRLMLDIOKOTAVEGEIEVNCCTAMASKPATITIRPFKNKELKXKSEVEEWSDM 201
QY 181 YTVTSQMLKVKHEDDGPVTCQVEHPAVTGNLQOTQRYLEVQYKPYQHIOMTYPLQGLTR 240
Db 202 YTVTSQMLKVKHEDDGPVTCQVEHPAVTGNLQOTQRYLEVQYKPYQHIOMTYPLQGLTR 261
QY 241 EGDAPFELTCEAIGKQPPVMTWVAVDDEMPQHAVLGSPNLFINNLTNGTGRCEASNI 300
Db 262 EGDAPFELTCEAIGKQPPVMTWVAVDDEMPQHAVLGSPNLFINNLTNGTGRCEASNI 321
QY 301 VGKASDYMALVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHA 360
Db 322 VGKASDYMALVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHA 381
QY 361 GVAVVAVFAMLCILIIIGRYFARHKGTYFTHKAGADADADADATAIINAGGONNSEKK 420
Db 382 GVAVVAVFAMLCILIIIGRYFARHKGTYFTHKAGADADADADATAIINAGGONNSEKK 441
QY 421 EYF 423
Db 442 EYF 444

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RESULT 2

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Q8K3T6 PRELIMINARY; PRT; 445 AA.
ID Q8K3T6;
AC Q8K3T6;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Synaptic cell adhesion molecule 1.
GN IGSF4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/
RA Biederer T., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,
RT Sudhof T.C.;
RT "SynCAM, a synaptic adhesion molecule that drives synapse assembly.";
RT Science 0:0-0(2002).
RL EMBL; AF539424; AAND1614.1; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . ; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR003597; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; IGC2_3.
DR SMART; SM00408; IGC2_1.
DR PROSITE; PS50835; IG-LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 445 AA; 4866 MW; 5B36F23F1877497 CRC64;

```

Query Match 99.8%; Score 2193; DB 11; Length 445;
 Best Local Similarity 99.8%; Pred. No. 1.6e-177;
 Matches 423; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAPPGLRLRLRLRLRLRLSAAALIPFGDGNLFTKDVTVIEGEVATISCCVNSKSDSVIQLN 60
Db 22 AAPGLRLRLRLRLRLRLSAAALIPFGDGNLFTKDVTVIEGEVATISCCVNSKSDSVIQLN 81
QY 61 PNRCTIYFRDPRPKDSRFQQLNFSSELKVSILTVNISIDEGRYFCQLYTDPPQESYTTI 120
Db 82 PNRCTIYFRDPRPKDSRFQQLNFSSELKVSILTVNISIDEGRYFCQLYTDPPQESYTTI 141
QY 121 TVLPPRLMLDIOKOTAVEGEIEVNCCTAMASKPATITIRPFKNKELKXKSEVEEWSDM 180
Db 142 TVLPPRLMLDIOKOTAVEGEIEVNCCTAMASKPATITIRPFKNKELKXKSEVEEWSDM 201
QY 181 YTVTSQMLKVKHEDDGPVTCQVEHPAVTGNLQOTQRYLEVQYKPYQHIOMTYPLQGLTR 240
Db 202 YTVTSQMLKVKHEDDGPVTCQVEHPAVTGNLQOTQRYLEVQYKPYQHIOMTYPLQGLTR 261
QY 241 EGDAPFELTCEAIGKQPPVMTWVAVDDEMPQHAVLGSPNLFINNLTNGTGRCEASNI 300
Db 262 EGDAPFELTCEAIGKQPPVMTWVAVDDEMPQHAVLGSPNLFINNLTNGTGRCEASNI 321
QY 301 VGKASDYMALVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHA 360
Db 322 VGKASDYMALVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHA 381
QY 361 GVAVVAVFAMLCILIIIGRYFARHKGTYFTHKAGADADADADATAIINAGGONNSEKK 420
Db 382 GVAVVAVFAMLCILIIIGRYFARHKGTYFTHKAGADADADADATAIINAGGONNSEKK 441
QY 421 EYF 423
Db 442 EYF 444

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RESULT 3

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Q8R5M8 PRELIMINARY; PRT; 456 AA.
ID Q8R5M8;
AC Q8R5M8;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RAI175.
GN IGSF4 OR RAI175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC Momot T.;
RA "Biological function of RAI175, a new member of immunoglobulin super
RT family";
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB064265; BAB83501.2; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . ; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGC2_1.
DR PROSITE; PS50835; IG-LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 456 AA; 49787 MW; 322E866A4BC1C7F CRC64;

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Query Match 99.1%; Score 2176.5; DB 11; Length 456;
 Best Local Similarity 97.2%; Pred. No. 4.1e-176;
 Matches 422; Conservative 1; Mismatches 0; Indels 11; Gaps 1;

QY 1 AAPGLRLRLRLRLRLRLSAALIPFGDGNLFTKDVTVIGEVATISQVKNKSDSDSVIQLN 60
 DB 22 AAPGLRLRLRLRLRLSAALIPFGDGNLFTKDVTVIGEVATISQVKNKSDSDSVIQLN 81
 QY 61 PNRQITVFRDPRPLKDSRFQNLNFSSELKXSLTNVISISDEGRYFCQLYTDPQESYTTI 120
 DB 82 PNRQITVFRDPRPLKDSRFQNLNFSSELKXSLTNVISISDEGRYFCQLYTDPQESYTTI 141
 QY 121 TVLVPRRLMTDIOQDTAVGESEIEVNCTAMASKPATITRMFKNGKELKGSEVEWSDM 180
 DB 142 TVLVPRRLMTDIOQDTAVGESEIEVNCTAMASKPATITRMFKNGKELKGSEVEWSDM 201
 QY 181 YTVTSQMLKVKHKEDDGVVVICQVEHPAVTGNLQOTRYLEVQYKPVHIOQMTYPLQGLTR 240
 DB 202 YTVTSQMLKVKHKEDDGVVVICQVEHPAVTGNLQOTRYLEVQYKPVHIOQMTYPLQGLTR 261
 QY 241 EGDAPFLTCBAIGKQPVMVTVWRVDEMPQHAVLSGNLFINNLKNTDNGTYRCEASNI 300
 DB 262 EGDAPFLTCBAIGKQPVMVTVWRVDEMPQHAVLSGNLFINNLKNTDNGTYRCEASNI 321
 QY 301 VGKASDVMLYVYDPTTIPPTTT 349
 DB 322 VGKASDVMLYVYDPTTIPPTTT 381
 QY 350 TIGAVDAHVIGVAVVVFAMLCILLIGRYFARHKGTFTHEAKGADDAADATAIINA 409
 DB 382 TIGAVDAHVIGVAVVVFAMLCILLIGRYFARHKGTFTHEAKGADDAADATAIINA 441
 QY 410 EGGQNSEKKEKF 423
 DB 442 EGGQNSEKKEKF 455

RESULT 4

Q9BY67 PRELIMINARY; PRT; 442 AA.
 AC Q9BY67
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nectin-like protein 2.
 GN NECTN2
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.,
 RT "Cloning of a novel human cDNA encoding a member of the immunoglobulin
 RT superfamily.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF132811; AAF69029.1;
 DR Genew; HGNC:5951; IGSP4.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003585; Neurexin-like.
 DR Pfam; PF00047; IG_3.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGc2; 1.
 DR PROSITE; PS00835; IG LIKE; 3.
 KM Immunoglobulin domain.
 SQ SEQUENCE 442 AA; 48537 MW; 68183E3238735062 CRC64;

Query Match 98.6%; Score 2166; DB 4; Length 442;
 Best Local Similarity 98.6%; Pred. No. 3.1e-175;
 Matches 417; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGLRLRLRLRLRLRLSAALIPFGDGNLFTKDVTVIGEVATISQVKNKSDSDSVIQLN 60
 DB 19 AAPGLRLRLRLRLRLRLSAALIPFGDGNLFTKDVTVIGEVATISQVKNKSDSDSVIQLN 78
 QY 61 PNRQITVFRDPRPLKDSRFQNLNFSSELKXSLTNVISISDEGRYFCQLYTDPQESYTTI 120
 DB 79 PNRQITVFRDPRPLKDSRFQNLNFSSELKXSLTNVISISDEGRYFCQLYTDPQESYTTI 138
 QY 121 TVLVPRRLMTDIOQDTAVGESEIEVNCTAMASKPATITRMFKNGKELKGSEVEWSDM 180
 DB 139 TVLVPRRLMTDIOQDTAVGESEIEVNCTAMASKPATITRMFKNGKELKGSEVEWSDM 198
 QY 181 YTVTSQMLKVKHKEDDGVVVICQVEHPAVTGNLQOTRYLEVQYKPVHIOQMTYPLQGLTR 240
 DB 199 YTVTSQMLKVKHKEDDGVVVICQVEHPAVTGNLQOTRYLEVQYKPVHIOQMTYPLQGLTR 258
 QY 241 EGDAPFLTCBAIGKQPVMVTVWRVDEMPQHAVLSGNLFINNLKNTDNGTYRCEASNI 300
 DB 259 EGDAPFLTCBAIGKQPVMVTVWRVDEMPQHAVLSGNLFINNLKNTDNGTYRCEASNI 318
 QY 301 VGKASDVMLYVYDPTTIPPTTT 360
 DB 319 VGKASDVMLYVYDPTTIPPTTT 378
 QY 361 GVAVVVFAMLCILLIGRYFARHKGTFTHEAKGADDAADATAIINAEGQNSEKK 420
 DB 379 GVAVVVFAMLCILLIGRYFARHKGTFTHEAKGADDAADATAIINAEGQNSEKK 438
 QY 421 EYF 423
 DB 439 EYF 441

RESULT 5

Q7TNL1 PRELIMINARY; PRT; 417 AA.
 AC Q7TNL1
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nectin-like molecule 2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6; TISSUE=Brain;
 RA Shingai T., Ikeda W., Kakunaga S., Morimoto K., Takekuni K., Itoh S.,
 RA Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.,
 RT "Implications of nectin-like molecule
 RT 2/IGSF4/RA175/SGISF/TS/CL1/SyncAM1 in cell-cell adhesion and
 RT transmembrane protein localization in epithelial cells";
 DR J. Biol. Chem. 0:0-0(2003).
 DR EMBL; AY351388; AA002381.1;
 SQ SEQUENCE 417 AA; 45779 MW; 98500180037845C2 CRC64;

Query Match 92.3%; Score 2027; DB 11; Length 417;
 Best Local Similarity 93.4%; Pred. No. 1.8e-163;
 Matches 395; Conservative 0; Mismatches 0; Indels 28; Gaps 1;

QY 1 AAPGLRLRLRLRLRLRLSAALIPFGDGNLFTKDVTVIGEVATISQVKNKSDSDSVIQLN 60
 DB 22 AAPGLRLRLRLRLRLRLSAALIPFGDGNLFTKDVTVIGEVATISQVKNKSDSDSVIQLN 81
 QY 61 PNRQITVFRDPRPLKDSRFQNLNFSSELKXSLTNVISISDEGRYFCQLYTDPQESYTTI 120
 DB 82 PNRQITVFRDPRPLKDSRFQNLNFSSELKXSLTNVISISDEGRYFCQLYTDPQESYTTI 141
 QY 121 TVLVPRRLMTDIOQDTAVGESEIEVNCTAMASKPATITRMFKNGKELKGSEVEWSDM 180
 DB 142 TVLVPRRLMTDIOQDTAVGESEIEVNCTAMASKPATITRMFKNGKELKGSEVEWSDM 201

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QY 181 YTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQOTRYLEVQYKQVHIQMTYPIQGLTR 240
DB 202 YTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQOTRYLEVQYKQVHIQMTYPIQGLTR 261
QY 241 EGGAFELTCAIGKPPQVMTWVRVDEMPQHAVLSGPNLFNNKNTKNDNGYRCEASNI 300
DB 262 EGGAFELTCAIGKPPQVMTWVRVDEMPQHAVLSGPNLFNNKNTKNDNGYRCEASNI 321
QY 301 VGKASDYMMLVYDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEECTIGAVDHAIVG 360
DB 322 VGKASDYMMLVYDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEECTIGAVDHAIVG 353
QY 361 GVAVAVVFMMLCLLIIIGRYFARHKGTYFTHKAGDADADADTALINAGGONNSEKK 420
DB 354 GVAVAVVFMMLCLLIIIGRYFARHKGTYFTHKAGDADADADTALINAGGONNSEKK 413
QY 421 EYF 423
DB 414 EYF 416

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RESULT 6

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O8N2F4 PRELIMINARY; PRT; 443 AA.
AC O8N2F4;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein HEMBA1001879.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayaishi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RT "NH1 human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075502; BAC11657.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_3.
DR SMART; SM00409; IG_3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG-LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 443 AA; 48648 MW; 046B43AA156F6F64 CRC64;

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Query Match 92.0%; Score 2020.5; DB 4; Length 443;
Best Local Similarity 92.9%; Pred. No. 6; 9e-163;
Matches 394; Conservative 5; Mismatches 24; Indels 1; Gaps 1;
QY 1 AAPPGLRLRLLLLSAALIPITGQGNLFPTKDVTVIEGVAITSCVNSKSDSVIQLLN 60
DB 19 AAPPGLRLRLLLLSAALIPITGQGNLFPTKDVTVIEGVAITSCVNSKSDSVIQLLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQNLNPSSELSKVLNVSISDEGRFQCLYDPPQESYTTI 120
DB 79 PNRQTIYFRDPRPLKDSRFQNLNPSSELSKVLNVSISDEGRFQCLYDPPQESYTTI 138
QY 121 TVLVPRNLMIDIOKDTAVEGEIEVACTAMASRPATITWFKGNKELKSKSEVEWSDM 180
DB 139 TVLVPRNLMIDIOKDTAVEGEIEVACTAMASRPATITWFKGNKELKSKSEVEWSDM 198
QY 181 YTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQOTRYLEVQYKQVHIQMTYPIQGLTR 240
DB 199 YTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQOTRYLEVQYKQVHIQMTYPIQGLTR 258
QY 241 EGGAFELTCAIGKPPQVMTWVRVDEMPQHAVLSGPNLFNNKNTKNDNGYRCEASNI 300

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DB 259 EGDALFELTCAIGKPPQVMTWVRVDEMPQHAVLSGPNLFNNKNTKNDNGYRCEASNI 318
QY 301 VGKASDYMMLVYDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEECTIGAVDHAIVG 359
DB 319 VGKASDYMMLVYDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEECTIGAVDHAIVG 378
QY 360 GVAVAVVFMMLCLLIIIGRYFARHKGTYFTHKAGDADADADTALINAGGONNSEKK 419
DB 379 GVAVAVVFMMLCLLIIIGRYFARHKGTYFTHKAGDADADADTALINAGGONNSEKK 438
QY 420 KEYF 423
DB 439 KEYF 442

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RESULT 7

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O9D6E7 PRELIMINARY; PRT; 336 AA.
AC O9D6E7;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE 2900073G06R1K protein.
GN IGSF4 OR 2900073G06R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi U., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner J., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaudo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima U., Mazzarelli U., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wymshar-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 403:685-690(2001).
DR EMBL; AK013775; BAB28988.1; -
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0018347; F:calcium independent cell adhesion molecule . . . ; IDA.
DR GO; GO:0005515; F:protein binding; IPT.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG-LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 336 AA; 37157 MW; FP887FAFAEFDF120 CRC64;

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Query Match 74.2%; Score 1631; DB 11; Length 336;
Best Local Similarity 100.0%; Pred. No. 5; 3e-130;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 AAPGLRLRLRLRLRLRLSAALIPITGDDGQLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
Db 22 AAPGLRLRLRLRLRLRLSAALIPITGDDGQLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 81
QY 61 PNRQTIYFRDPRPLKDSRFQQLNFSSESLKVSILTNVSIISDEGRYFCQLYTDPPOSYTTI 120
Db 82 PNRQTIYFRDPRPLKDSRFQQLNFSSESLKVSILTNVSIISDEGRYFCQLYTDPPOSYTTI 141
QY 121 TVLVPRLMLTDIQKDTAVEGEIEIVNCTAMASKPATIIRFWKGNKELKGSEVEEWSDM 180
Db 142 TVLVPRLMLTDIQKDTAVEGEIEIVNCTAMASKPATIIRFWKGNKELKGSEVEEWSDM 201
QY 181 YTVTSQMLKVKHKEDDGVPIICQVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTR 240
Db 202 YTVTSQMLKVKHKEDDGVPIICQVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTR 261
QY 241 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVALSGPNLFINNLKNTDNGTYRCEASNI 300
Db 262 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVALSGPNLFINNLKNTDNGTYRCEASNI 321
QY 301 VGKAHSDYMLYVY 313
Db 322 VGKAHSDYMLYVY 334

RESULT 8
Q80VG4 ID 080VG4 PRELIMINARY; PRT; 336 AA.
AC 080VG4;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE A secretory form of SgISGF/TSIC1.
GN SgISGF/TSIC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Spleen cell-derived;
RA Ito A., Koma Y., Nagano T.;
RT "A secretory form of SgISGF/TSIC1."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092414; BAC66173.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_3.
DR SMART; SM00409; IGc2; 3.
DR PROSITE; PSS0835; IG_LIKE; 3.
SQ SEQUENCE 336 AA; 37155 MW; 9EF3D8B8BE5E8F72 CRC64;

Query Match 74.2%; Score 1631; DB 11; Length 336;
Best Local Similarity 100.0%; Pred. No. 5.3e-130;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVALSGPNLFINNLKNTDNGTYRCEASNI 300
Db 262 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVALSGPNLFINNLKNTDNGTYRCEASNI 321
QY 301 VGKAHSDYMLYVY 313
Db 322 VGKAHSDYMLYVY 334

RESULT 9
Q86WB8 ID 086WB8 PRELIMINARY; PRT; 333 AA.
AC 086WB8;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Secretory isoform of TSIC-1.
GN TSIC-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Ito A., Koma Y., Nagano T.;
RT "Cloning of a secretory isoform of SgISGF/TSIC-1."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB094146; BAC66178.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_3.
DR SMART; SM00409; IG_3.
DR SMART; SM00408; IGc2; 3.
DR PROSITE; PSS0835; IG_LIKE; 3.
SQ SEQUENCE 333 AA; 36915 MW; D7C1102F46D08492 CRC64;

Query Match 73.5%; Score 1615; DB 4; Length 333;
Best Local Similarity 99.0%; Pred. No. 1.2e-128;
Matches 310; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 AAPGLRLRLRLRLRLRLSAALIPITGDDGQLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
Db 19 AAPGLRLRLRLRLRLRLSAALIPITGDDGQLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQQLNFSSESLKVSILTNVSIISDEGRYFCQLYTDPPOSYTTI 120
Db 79 PNRQTIYFRDPRPLKDSRFQQLNFSSESLKVSILTNVSIISDEGRYFCQLYTDPPOSYTTI 138
QY 121 TVLVPRLMLTDIQKDTAVEGEIEIVNCTAMASKPATIIRFWKGNKELKGSEVEEWSDM 180
Db 139 TVLVPRLMLTDIQKDTAVEGEIEIVNCTAMASKPATIIRFWKGNKELKGSEVEEWSDM 198
QY 181 YTVTSQMLKVKHKEDDGVPIICQVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTR 240
Db 199 YTVTSQMLKVKHKEDDGVPIICQVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVALSGPNLFINNLKNTDNGTYRCEASNI 300
Db 259 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVALSGPNLFINNLKNTDNGTYRCEASNI 318
QY 301 VGKAHSDYMLYVY 313
Db 319 VGKAHSDYMLYVY 331

RESULT 10
Q92ZB8 ID 092ZB8 PRELIMINARY; PRT; 295 AA.
AC 092ZB8;
DT 01-MAY-1999 (Tremblrel. 10, Created)

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DT 01-MAY-1999 (T-EMBLrel. 10, last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)
 DE Nectin-like protein 2.
 GN IGSF4 OR NECT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX [1]
 RN SEQUENCE FROM N.A.
 RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
 RT "Cloning of a novel cDNA encoding a member of immunoglobulin-like
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF061260; AAC67243.1; -
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; F:protein binding; IPT.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32509 MW; 9DE9D86F6F648 CRC64;
 Query Match 70.4%; Score 1546; DB 11; Length 295;
 Best Local Similarity 100.0%; Pred. No. 7.2e-123;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 MIDIQKTAVGEIEVNCCTAMASKPATITRMFKGNKELKGKSEVEEWSMDYVTSQML 189
 DB 1 MIDIQKTAVGEIEVNCCTAMASKPATITRMFKGNKELKGKSEVEEWSMDYVTSQML 60
 QY 190 KVHKEDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTRGDAPFLTC 249
 DB 61 KVHKEDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTRGDAPFLTC 120
 QY 250 EAIKGPQVMTWVRVDDEMPQHAVALSGPNLFINLNKNTNGTYRCASNIIVGKASDYM 309
 DB 121 EAIKGPQVMTWVRVDDEMPQHAVALSGPNLFINLNKNTNGTYRCASNIIVGKASDYM 180
 QY 310 LYVVDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIVGVAVVFA 369
 DB 181 LYVVDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIVGVAVVFA 240
 QY 370 MLCILITLGRYFAHKGTYFTHAKGADDAADDTALINAEQGNSEEKKEVF 423
 DB 241 MLCILITLGRYFAHKGTYFTHAKGADDAADDTALINAEQGNSEEKKEVF 294
 RESULT 11
 QOXYL4 PRELIMINARY; PRT; 306 AA.
 ID 09OYL4
 AC 09OYL4
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)
 DE Adhesion protein RAI75C.
 GN IGSF4 OR RAI75C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX [1]
 RN SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kourouku Y., Momoi M.,
 Momoi T.;

RT "RAI75, a novel neuron specific adhesion protein.",
 RL Submitted (Dec-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021966; BAA87916.1; -
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; F:protein binding; IPT.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 306 AA; 33522 MW; A4CE37B0F2354D5 CRC64;
 Query Match 68.9%; Score 1513.5; DB 11; Length 306;
 Best Local Similarity 95.4%; Pred. No. 4.3e-120;
 Matches 291; Conservative 1; Mismatches 2; Indels 11; Gaps 1;
 QY 130 MIDIQKTAVGEIEVNCCTAMASKPATITRMFKGNKELKGKSEVEEWSMDYVTSQML 189
 DB 1 MIDIQKTAVGEIEVNCCTAMASKPATITRMFKGNKELKGKSEVEEWSMDYVTSQML 60
 QY 190 KVHKEDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTRGDAPFLTC 249
 DB 61 KVHKEDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTRGDAPFLTC 120
 QY 250 EAIKGPQVMTWVRVDDEMPQHAVALSGPNLFINLNKNTNGTYRCASNIIVGKASDYM 309
 DB 121 EAIKGPQVMTWVRVDDEMPQHAVALSGPNLFINLNKNTNGTYRCASNIIVGKASDYM 180
 QY 310 LYVVDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIV 358
 DB 181 LYVVDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIV 240
 QY 359 IGVAVVAVVFMCLLITLGRYFAHKGTYFTHAKGADDAADDTALINAEQGNSEE 428
 DB 241 IGVAVVAVVFMCLLITLGRYFAHKGTYFTHAKGADDAADDTALINAEQGNSEE 300
 QY 419 KKEVF 423
 DB 301 KKEVF 305
 RESULT 12
 QOXYL6 PRELIMINARY; PRT; 295 AA.
 ID 09OYL6
 AC 09OYL6
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)
 DE Adhesion protein RAI75A.
 GN IGSF4 OR RAI75A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX [1]
 RN SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kourouku Y., Momoi M.,
 Momoi T.;

DR GO; GO:0005515; F:protein binding; IPT.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003585; Neurexin-like.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SMART0294; 4.1m; 1.
 DR SMART; SMART0408; IGC2; 1.
 DR PROSITE; PSS0835; IG-LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32347 MW; FDD9B8145C6B971B CRC64;

Query Match 68.0%; Score 1493; DB 11; Length 295;
 Best Local Similarity 96.6%; Pred. No. 2,3e-118;
 Matches 284; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 130 MIDIQDVAEGEIEVNCTAMASKPATIRPFKNKELKSGSEVEEMSDMYTVTSQML 189
 DB 1 MIDIQDVAEGEIEVNCTAMASKPATIRPFKNKELKSGSEVEEMSDMYTVTSQML 60
 QY 190 KVHKEDDGVPIQVYEHPAVGNLQTORYLEVQYKPOVHIQMTYPLQGLTRGDALFELTC 249
 DB 61 KVHKEDDGVPIQVYEHPAVGNLQTORYLEVQYKPOVHIQMTYPLQGLTRGDALFELTC 120
 QY 250 EAIGKQPVMVTVWRVDEMPQHAVLSGNLFINNLTNDNGTYCEASNIYGAHSDYM 309
 DB 121 EAIGKQPVMVTVWRVDEMPQHAVLSGNLFINNLTNDNGTYCEASNIYGAHSDYM 180
 QY 310 LVYVDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTSDSAGEEGTIGAVDHAVIGVAVVVA 369
 DB 181 LVYVDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTSDSAGEEGTIGAVDHAVIGVAVVVA 240
 QY 370 MCLLIILIGRYFARHKGTYFTHAKGADDAADADTAIINAGGQNNSEKKEYF 423
 DB 241 MCLLIILIGRYFARHKGTYFTHAKGADDAADADTAIINAGGQNNSEKKEYF 294

RESULT 13

Q9QYL5 PRELIMINARY; PRT; 289 AA.
 AC Q9QYL5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI75B.
 GN IGSF4 OR RAI75B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kourouku Y., Momoi M.,
 RA Momoi T.;
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL, AB021965; BAA87915.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; F:protein binding; IPT.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003585; Neurexin-like.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SMART0294; 4.1m; 1.
 DR SMART; SMART0408; IGC2; 1.
 DR PROSITE; PSS0835; IG-LIKE; 2.
 KW Immunoglobulin domain.

SQ SEQUENCE 289 AA; 31811 MW; 8D1B836D0565AE4 CRC64;

Query Match 63.9%; Score 1404; DB 11; Length 289;
 Best Local Similarity 92.5%; Pred. No. 7.9e-111;
 Matches 272; Conservative 2; Mismatches 14; Indels 6; Gaps 1;

QY 130 MIDIQDVAEGEIEVNCTAMASKPATIRPFKNKELKSGSEVEEMSDMYTVTSQML 189
 DB 1 MIDIQDVAEGEIEVNCTAMASKPATIRPFKNKELKSGSEVEEMSDMYTVTSQML 60
 QY 190 KVHKEDDGVPIQVYEHPAVGNLQTORYLEVQYKPOVHIQMTYPLQGLTRGDALFELTC 249
 DB 61 KVHKEDDGVPIQVYEHPAVGNLQTORYLEVQYKPOVHIQMTYPLQGLTRGDALFELTC 120
 QY 250 EAIGKQPVMVTVWRVDEMPQHAVLSGNLFINNLTNDNGTYCEASNIYGAHSDYM 309
 DB 121 EAIGKQPVMVTVWRVDEMPQHAVLSGNLFINNLTNDNGTYCEASNIYGAHSDYM 180
 QY 310 LVYVDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTSDSAGEEGTIGAVDHAVIGVAVVVA 369
 DB 181 LVYVDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTSDSAGEEGTIGAVDHAVIGVAVVVA 234
 QY 370 MCLLIILIGRYFARHKGTYFTHAKGADDAADADTAIINAGGQNNSEKKEYF 423
 DB 235 MCLLIILIGRYFARHKGTYFTHAKGADDAADADTAIINAGGQNNSEKKEYF 288

RESULT 14

Q9QYL3 PRELIMINARY; PRT; 278 AA.
 AC Q9QYL3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI75N.
 GN IGSF4 OR RAI75N.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kourouku Y., Momoi M.,
 RA Momoi T.;
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL, AB021967; BAA87917.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; F:protein binding; IPT.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003585; Neurexin-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SMART0294; 4.1m; 1.
 DR SMART; SMART0408; IGC2; 1.
 DR PROSITE; PSS0835; IG-LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 278 AA; A295F4DEA2724B04 CRC64;

Query Match 62.8%; Score 1380.5; DB 11; Length 278;
 Best Local Similarity 90.8%; Pred. No. 7.4e-109;
 Matches 267; Conservative 2; Mismatches 8; Indels 17; Gaps 1;

QY 130 MIDIQDVAEGEIEVNCTAMASKPATIRPFKNKELKSGSEVEEMSDMYTVTSQML 189
 DB 1 MIDIQDVAEGEIEVNCTAMASKPATIRPFKNKELKSGSEVEEMSDMYTVTSQML 60
 QY 190 KVHKEDDGVPIQVYEHPAVGNLQTORYLEVQYKPOVHIQMTYPLQGLTRGDALFELTC 249

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Db      61 KHKEDDGVVICQVEHPATGSLQTORYLEVQYKQVHIQMTYPLQGLTREGDALLFLTC 120
Qy      250 EAIGKPOVWNTWVRVDDDEMPQHAVISGNPLFTNNLNKTDNGTYRCEASNTYKASHSDY 309
Db      121 EAIGKPOVWNTWVRVDDDEMPQHAVISGNPLFTNNLNKTDNGTYRCEASNTYKASHSDI 180
Qy      310 LYYVDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 369
Db      181 LYYVD-----TTATTPRAVHNSRAGEGCTICAVDHAVIGGVAVVFA 223
Qy      370 MCLLLILGRYFARHKGTFTTHEAKGADDAADTAIINAEQQNNSEKKEYF 423
Db      224 MCLLLILGRYFARHKGTFTTHEAKGADDAADTAIINAEQQNNSEKKEYF 277

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Qy      350 TIGAVDHAVIGGVAVVVFAMLCILLILGRYFARHKGTFTTHEAKGADDAADTAIINA 409
Db      365 P---DHALIGGIYAVVVFVTLCSIFILGRYLARHKGTFTTHEAKGADDAADTAIINA 420
Qy      410 EGGQNNSEKKEYF 423
Db      421 EGGQNNSEKKEYF 434

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Search completed: July 7, 2004, 06:02:45
Job time : 60.1711 secs

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RESULT 15
Q8N3J6 PRELIMINARY; PRT; 435 AA.
ID Q8N3J6
AC Q8N3J6;
DT 01-OCT-2002 (TremBrel. 22, Created)
DT 01-OCT-2002 (TremBrel. 22, Last sequence update)
DT 01-OCT-2002 (TremBrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKFZP761G128.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Amygdala;
RA Koehler K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834270; CAD38345.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGG2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 435 AA; 47554 MW; 59DD41B7F34D446 CRC64;

```

Query Match 40.8%; Score 897; DB 4; Length 435;
Best Local Similarity 44.2%; Pred. No. 1.5e-67;
Matches 192; Conservative 75; Mismatches 139; Indels 28; Gaps 7;

```

Qy      11 LLLLSAALIFPG-DGONLFTKDVTVIEGEVATISCOVNSDDSVIQLINPRQTIYFR 69
Db      8 VLRFSYVCGLLIGSQSQQFPILTQNTVYVEGTAIILTCRVQNDNTSLQWNSNPAQTLTFD 67
Qy      70 DFRPLKDSRFQLNFSSESEKSLFTNVSISDEGRYFCQLYTDPPQESYTTIYLVPPRL 129
Db      68 DKKALRDNRILELVAWSHELISIVSDVLSDEGQYCSLFTMPVKTSKAYLIVLGVBEKP 127
Qy      130 MIDQKTVAGEIEIENCTAMASKPATITRMFKGNKELKGSVEEWS---DMYTVTSQ 186
Db      128 QISGSSPWEKEDLMQLCTKTSKSPADIRWFQNDKEIKDVYIKLKEDANRKTFTYSS 187
Qy      187 LMLVHKEDDGVVICQVEHPATGSLQTORYLEVQYKQVHIQMTYPLQGLTREGDAF 245
Db      188 LDFRVDSDDGVAVICRVDSHSLNATPQVAMQVLEIHYTPSVK---IPSTPPQEGQPL 244
Qy      246 ELTCEAIGKPOVWNTWVRVDDDEMPQHAVISGNPLFTNNLNKTDNGTYRCEASNTYK 303
Db      245 ILTCESEKGPLFEVPLMTKGGELPDPKRWVSGREINILFLNKTDNGTYRCEATNTIGQ 304
Qy      304 AHSQVMLVYVDPPTTPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 349
Db      305 SSAEYVILVHVNTLPLPTTIIPLTATVTTVAITTSPTTSATSSIRDPNALAQNG 364

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QY 121 TLVPPNLMIDIOKTAVEGESEIEVNCMTAMASKPATITRMKPKNELKKGSEVEEMSDM 180
    |||
Db 139 TLVPPNLMIDIOKTAVEGESEIEVNCMTAMASKPATITRMKPKNELKKGSEVEEMSDM 198
QY 181 YTTVTSQMLKXHKEDSGVPVICOVEHPAVTGNLQTOEYLEVOYKPOVHIQMTYPLQGLTR 240
    |||
Db 199 YTTVTSQMLKXHKEDSGVPVICOVEHPAVTGNLQTOEYLEVOYKPOVHIQMTYPLQGLTR 258
QY 241 EGDGFELTCEAIGPCQVMTWVAVDEMPQAHLSGPNLFINNKNTDNGTCRCAASNT 300
    |||
Db 259 EGDGFELTCEAIGPCQVMTWVAVDEMPQAHLSGPNLFINNKNTDNGTCRCAASNT 318
QY 301 VGKASDYMLYVDPPTTIPPTTTTTTTTTTTTTTTTTITDTSRAGEEGTIGAVDAVIG 360
    |||
Db 319 VGKASDYMLYVDPPTTIPPTTTTTTTTTTTTTTTTTITDTSRAGEEGSIRAVDAVIG 378
QY 361 GVAVAVVFAMLCILITIGRFARHKGYTFTHAKGADADADADTAIINAGGONNSEBK 420
    |||
Db 379 GVAVAVVFAMLCILITIGRFARHKGYTFTHAKGADADADADTAIINAGGONNSEBK 438
QY 421 EYF 423
    |||
Db 439 EYF 441

RESULT 3
AAV94341
ID AAV94341 standard; protein; 442 AA.
XX
AC AAV94341;
XX
DT 22-AUG-2000 (first entry)
DE Human cell surface receptor protein #8.
XX
XX Human; HCSR; cytostatic; antiarthritic; antirheumatic; antiaesthetic;
KW immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic;
KW neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma;
KW rheumatoid arthritis; asthma; atherosclerosis; akathesia;
KW Alzheimer's diseases; multiple sclerosis; epilepsy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..44
FT /label= Signal_peptide
FT Protein 45..442
FT /label= HCSR-8
FT Region 53
FT /note= "potential phosphorylation site"
FT Domain 57..126
FT /label= Immunoglobulin_domain
FT Region 67
FT /note= "potential glycosylation site"
FT Region 101
FT /note= "potential glycosylation site"
FT Region 103
FT /note= "potential phosphorylation site"
FT Region 113
FT /note= "potential glycosylation site"
FT Region 115
FT /note= "potential glycosylation site"
FT Region 155
FT /note= "potential phosphorylation site"
FT Domain 159..222
FT /label= Immunoglobulin_domain
FT Region 165
FT /note= "potential glycosylation site"
FT Region 176
FT /note= "potential phosphorylation site"
FT Region 190
FT /note= "potential phosphorylation site"
FT Region 233

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FT /note= "potential phosphorylation site"
FT Region 241
FT /note= "potential phosphorylation site"
FT Domain 260..315
FT /label= Immunoglobulin_domain
FT Region 304
FT /note= "potential glycosylation site"
FT Region 308
FT /note= "potential glycosylation site"
FT Region 310
FT /note= "potential phosphorylation site"
FT Region 329
FT /note= "potential phosphorylation site"
FT Region 368
FT /note= "potential phosphorylation site"
FT Domain 375..394
FT /label= Transmembrane_domain
FT Region 432
FT /note= "potential glycosylation site"

MO200028032-A2.
PD 18-MAY-2000.
XX
PF 12-NOV-1999; 99WO-US026742.
XX
PR 12-NOV-1998; 98US-00191280.
PR 07-DEC-1998; 98US-00206647.
PR 08-MAR-1999; 99US-0123404P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YF, Corley NC, Guegler KJ, Yue H, Baughn MR, Lal P;
PI Hillman JL, Bandman O, Azimzai Y, Au-Young J;
DR WPI: 2000-376546/32.
DR N-PSDB: AAA27051.
XX
PT New human cell surface receptor protein and polynucleotide useful for
PT diagnosis, prevention and treatment of cancer, immune disorders,
PT infection and neuronal disorders.
XX
PS Claim 1; Page 61-82; 97pp; English.
XX
CC The present sequence is a novel human cell surface receptor protein
CC (HCSR) designated HCSR-8. The nucleotide sequence was identified in
CC Incyte Clone 312256 from the cDNA library LUNG0702, which was made from
CC RNA isolated from lung tissue. A number of Incyte Clones were used to
CC assemble the consensus sequence. BLAST analysis showed that the sequence
CC is homologous to immunosuppressant protein B12 g3779242. HCSR and its
CC antagonist are useful for preventing or treating disorders associated
CC with decreased or increased expression or activity of HCSR. Such
CC disorders include cancer such as leukaemia and melanoma, immune
CC disorders such as rheumatoid arthritis, asthma and atherosclerosis,
CC bacterial and parasitic infections and neuronal disorders such as
CC akathesia, Alzheimer's disease, multiple sclerosis and epilepsy.
CC Polynucleotides encoding HCSR may be used as hybridisation probes to
CC diagnose these conditions. Anti-HCSR antibodies may be used as
CC antagonists, as a targeting or delivery mechanism for bringing
CC pharmaceutical agents into contact with cells or tissues expressing HCSR
CC and for diagnosis of HCSR-related disorders. HCSR and its catalytic or
CC immunogenic fragments are useful for drug screening using libraries of
CC compounds.
XX
SQ Sequence 442 AA;
XX
Query Match 98.7%; Score 2169; DB 3; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.1e-149;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 AAPGLRLRLILLISAAALPTGDDGNTLFTKDVTVIGEVATISCOVNSDDSVIOLN 60
Db 19 AAPGLRLRLILLISAAALPTGDDGNTLFTKDVTVIGEVATISCOVNSDDSVIOLN 78

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QY 61 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSITNVSISDEGRYFCQLYTDPPOESYTTI 120
DB 79 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSITNVSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVVPPRNLMTDIOKDTAVEGEIEVNCJAMASKPATITIRFKGNKELKSGSEVEMSDM 180
DB 139 TVVPPRNLMTDIOKDTAVEGEIEVNCJAMASKPATITIRFKGNKELKSGSEVEMSDM 198
QY 181 YTVTSQMLKVKHKEDDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHKEDDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEALIGRPOPMVTWVRVDEMPQHAVALSGPNLFINNKNTDNGTRCEASNI 300
DB 259 EGDAPFELTCEALIGRPOPMVTWVRVDEMPQHAVALSGPNLFINNKNTDNGTRCEASNI 318
QY 301 VGKASDYMVLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIVG 360
DB 319 VGKASDYMVLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGSIRAVDHAIVG 378
QY 361 GVAVVAVVPMCLIIIGRYFARHKGYFTHEAKGADDAADADATAIINAGGQNNSEKK 420
DB 379 GVAVVAVVPMCLIIIGRYFARHKGYFTHEAKGADDAADADATAIINAGGQNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 4
AAV45092
ID AAV45092 standard; protein; 442 AA.
AC AAV45092;
DT 31-MAY-2000 (first entry)
DE Human lymphoid derived dendritic cell adhesion molecule.
XX
XX Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-1;
XX B7-1; T cell proliferation; natural killer cell; NK; tumour cell;
XX biological activity; quality control reagent; treatment; inflammation;
XX immune system disorder; autoimmune; viral infection; infectious disease;
XX organ transplant rejection; bone marrow; modulator; immune response.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
XX Key 1..374
XX Domain /label= Extracellular_domain
XX Peptide 1..38
XX Protein /label= Leader_peptide
XX Modified-site 39..442
XX /label= Mature_human_LDCAM_polypeptide
XX /note= 67..69
XX /note= "N-Glycosylation site"
XX Modified-site 101..103
XX /note= "N-Glycosylation site"
XX Modified-site 113..115
XX /note= "N-Glycosylation site"
XX Modified-site 165..167
XX /note= "N-Glycosylation site"
XX Modified-site 304..306
XX /note= "N-Glycosylation site"
XX Modified-site 308..310
XX /note= "N-Glycosylation site"
XX Domain /note= "N-Glycosylation site"
XX /label= Transmembrane_domain
XX /label= 396..442
XX /label= Cytoplasmic_domain
XX
XX WO200008158-A2.

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XX 17-FEB-2000.
XX 05-AUG-1999; 99KO-US017905.
XX 07-AUG-1998; 98US-0095672P.
XX (IMMV ) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC;
XX WPI: 2000-205712/18.
XX N-PSDB; AA250882.
XX
XX Novel molecules designated LDCAM are capable of altering or modulating T
XX cell function.
XX
XX Claim 7; Page 42-43; 44pp; English.
XX
XX The present amino acid sequence is the human lymphoid derived dendritic
XX cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic
XX cells and displays homology to adhesion molecules, B7-1 and cytoplasmic
XX region of B7-1. Human LDCAM is expressed in breast, retina, foetal
XX liver, spleen and heart, lung, muscle, placenta, thymoid and lung
XX carcinoma. LDCAM polypeptides interact with T cell surface molecules to
XX alter signalling and inhibits T cell proliferation, bind to themselves
XX and B7-1, an LDCAM binding protein and increases natural killer (NK)
XX cell populations. It may be used to measure the biological activity and
XX as quality control reagents of LDCAM binding proteins. LDCAM may be used
XX for treating disorders associated with malfunctioning of immune system,
XX inflammation, autoimmune disorders, viral infected cells, infectious
XX diseases and for killing tumour cells. They are also useful for
XX prevention or reducing the effect of organ and bone marrow transplant
XX rejection and for modulating T cell immune response. LDCAM polypeptides
XX may also be used as carriers for delivering agents attached to T cells or
XX cells bearing B7-1
XX
XX Sequence 442 AA:
XX
XX Query Match 98.7%; Score 2169; DB 3; Length 442;
XX Best Local Similarity 98.8%; Pred. No. 2,1e-149;
XX Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 AAPGLRLRLILLLLSAAALIPDGGQLFTKDYTVIEGVATISCVNKSDDSVIQLN 60
XX 19 AAPGLRLRLILLLLSAAALIPDGGQLFTKDYTVIEGVATISCVNKSDDSVIQLN 78
DB
QY 61 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSITNVSISDEGRYFCQLYTDPPOESYTTI 120
DB 79 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSITNVSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVVPPRNLMTDIOKDTAVEGEIEVNCJAMASKPATITIRFKGNKELKSGSEVEMSDM 180
DB 139 TVVPPRNLMTDIOKDTAVEGEIEVNCJAMASKPATITIRFKGNKELKSGSEVEMSDM 198
QY 181 YTVTSQMLKVKHKEDDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHKEDDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEALIGRPOPMVTWVRVDEMPQHAVALSGPNLFINNKNTDNGTRCEASNI 300
DB 259 EGDAPFELTCEALIGRPOPMVTWVRVDEMPQHAVALSGPNLFINNKNTDNGTRCEASNI 318
QY 301 VGKASDYMVLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIVG 360
DB 319 VGKASDYMVLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGSIRAVDHAIVG 378
QY 361 GVAVVAVVPMCLIIIGRYFARHKGYFTHEAKGADDAADADATAIINAGGQNNSEKK 420
DB 379 GVAVVAVVPMCLIIIGRYFARHKGYFTHEAKGADDAADADATAIINAGGQNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

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Db 439 EYF 441

RESULT 5
AAE19887
ID AAE19887 standard; protein, 442 AA.
XX
XX AAE19887;
AC
AC AAE19887;
DT 18-JUN-2002 (first entry)
XX
XX Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.
DE
XX Human; hepatocellular carcinoma; tumour suppressor lung cancer 1; TSLC1;
KM liver; lung; pancreatic cancer; cell proliferative disorder; cytostatic;
KM gene therapy.
XX
XX Homo sapiens.
OS
XX WO200214557-A1.
PN
XX 21-FEB-2002.
PD
XX 15-AUG-2001; 2001WO-US025690.
PF
XX 15-AUG-2000; 2000US-0225264P.
PR
XX (UYUO) UNITV JOHNS HOPKINS SCHOOL MEDICINE.
PA
XX Reeves RH, Yoshinori M;
XX
XX WPI; 2002-241913/29.
DR
XX
XX WPI; 2002-241913/29.
PT
XX Detecting cell proliferative disorder associated with tumor suppressor
PT lung cancer (TSLC) 1 in subject, comprises contacting proliferating cell
PT of subject with reagent detecting TSLC1 and detecting modification in
PT TSLC1 level.
XX
XX
XX Disclosure; Page 49-50; 59pp; English.
PS
XX
XX The invention relates to a method for detecting cell proliferative
CC disorder associated with tumour suppressor lung cancer 1 (TSLC1) in a
CC subject. The method comprising contacting a cell component of a
CC proliferating cell with a reagent that detects level of the cell
CC component in the proliferating cell and determining modification in the
CC level of the cell component in proliferating cell as compared with a
CC healthy cell, where modification indicates disorder associated with a
CC TSLC1. The method is useful for detecting a cell proliferative disorder
CC (e.g. liver, lung or pancreatic cancer) associated with tumour suppressor
CC lung cancer 1 (TSLC1) in a subject. The invention is useful in gene
CC therapy and for treating a cell proliferative disorder such as lung
CC cancer (human non-small cell lung cancer), liver cancer (hepatocellular
CC carcinoma) or pancreatic cancer associated with modification of TSLC1
CC production, where a reagent which modulates (preferably, increases) TSLC1
CC level in the cells, is employed. The present sequence is human TSLC1
XX
XX
SQ Sequence 442 AA;
Query Match 98.7%; Score 2169; DB 5; Length 442;
Best Local Similarity 98.8%; Pred. No 2,1e-149;
Matches 416; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 181 YTVTSQMLKVKHEDDGVVICQVHPAVTGNLQTORYLEVOYKQPOVHIOMTYPIQGLTR 240
|||
Db 199 YTVTSQMLKVKHEDDGVVICQVHPAVTGNLQTORYLEVOYKQVHLOMYPIQGLTR 258
|||
QY 241 ESDAFELTCEAIGKQPPVWTVWRYVDDEMPQHAVISGPNLFINNKTNDNGTYRCEASNI 300
|||
Db 259 ESDAFELTCEAIGKQPPVWTVWRYVDDEMPQHAVISGPNLFINNKTNDNGTYRCEASNI 318
|||
QY 301 VGRASDVMLYVYDPTTTPPTTT 360
|||
Db 319 VGRASDVMLYVYDPTTTPPTTT 378
|||
QY 361 GVAVVVFAMLCILLIGRYFARHKGTYFTHKAGADDAADATIAINAGGQNNSEEXK 420
|||
Db 379 GVAVVVFAMLCILLIGRYFARHKGTYFTHKAGADDAADATIAINAGGQNNSEEXK 438
|||
QY 421 EYF 423
|||
Db 439 EYF 441

RESULT 6
ABP62825
ID ABP62825 standard; protein, 442 AA.
XX
XX ABP62825;
AC
XX 14-OCT-2002 (first entry)
DT
XX
XX Human polypeptide SEQ ID NO 262.
DE
XX
XX Human; vulnereary; dermatological; neuroprotective; noctropic; cancer;
KM antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
KM antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
KM burn; central nervous system disorder; Alzheimer's disease;
KM Parkinson's disease; Huntington's disease; immune disorder;
KM autoimmune disorder; multiple sclerosis; diabetes; allergy.
XX
XX Homo sapiens.
OS
XX
XX WO200218424-A2.
PN
XX 07-MAR-2002.
PD
XX
XX 31-AUG-2001; 2001WO-US027093.
PF
XX
XX 01-SEP-2000; 2000US-00654935.
PR
XX (HYSE-) HYSEQ INC.
PA
XX
XX Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
PI Zhao QA, Wang D, Liu C, Drmanac RT, Weinman T;
PI WPI; 2002-583321/62.
DR N-PSDB; ABQ93304.
XX
XX
XX New polynucleotide and polypeptides, useful for treatment and diagnosis
PT of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
PT sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
PT sclerosis, diabetes and allergies.
XX
XX Claim 20; SEQ ID NO 262; 284pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising one of
CC 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising
CC administering to a mammalian subject a composition comprising the protein
CC (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
CC (II), (II) and (III) are useful for diagnostic evaluation of disorders.
CC (I) is useful for gene therapy of diseases and (II) can be used for
CC therapeutic treatment. Diseases that may be treated include wound healing
CC and tissue repair, burns, central nervous system disorders (e.g.
CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral

CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 CC sclerosis, diabetes and allergies. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 442 AA:

Query Match 98.7%; Score 2169; DB 5; Length 442;
 Best Local Similarity 98.8%; Pred. No. 2.1e-149;
 Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGRLRLRLLLLSAALIPFGDGNLFKQDVTVEGEVATISGVNKSDDSVIQLN 60
 DB 19 AAPGRLRLRLLLLSAALIPFGDGNLFKQDVTVEGEVATISGVNKSDDSVIQLN 78
 QY 61 PNRQTIYFRDPRPLKDSRFQNLNFSSELKSLTNVISDEGRYFCQLYTDPQESYTTI 120
 DB 79 PNRQTIYFRDPRPLKDSRFQNLNFSSELKSLTNVISDEGRYFCQLYTDPQESYTTI 138
 QY 121 TLVPPRNLMIDIQKQTAVEGEIEVNCTAMASKPATTTIRFKGNTELKGSVEEWSDM 180
 DB 139 TLVPPRNLMIDIQKQTAVEGEIEVNCTAMASKPATTTIRFKGNTELKGSVEEWSDM 198
 QY 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTR 240
 DB 199 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTR 258
 QY 241 EGDAPFETGALGKPPQVMTWTRVDDENPQHAVLSEGNLFINLNKLTNGYTRCASNI 300
 DB 259 EGDAPFETGALGKPPQVMTWTRVDDENPQHAVLSEGNLFINLNKLTNGYTRCASNI 318
 QY 301 VGNKSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDAVVG 360
 DB 319 VGNKSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDAVVG 378
 QY 361 GVAVAVVFAMLCILIIIGRYFARHKGTYFTEAKGADDAADTAIINAGGONNSEKK 420
 DB 379 GVAVAVVFAMLCILIIIGRYFARHKGTYFTEAKGADDAADTAIINAGGONNSEKK 438
 QY 421 EYF 423
 DB 439 EYF 441

RESULT 7
 ADA27144
 ID ADA27144 standard; protein; 442 AA.
 XX
 AC ADA27144;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human novel secreted protein from gene 11 #3.
 XX
 KM cytosolic; antiinflammatory; immunomodulator; neuroprotective;
 KM hemostatic; gene therapy; cancer; inflammation; immune disorder;
 KM neurological disorder; blood clotting disorder; food additive;
 KM preservative; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN US2003055231-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 29-OCT-2001; 2001US-00984130.
 XX
 PR 28-OCT-1998; 98US-0105971P.
 PR 27-OCT-1998; 99WO-US025031.
 PR 19-APR-2000; 2000US-0198407P.
 PR 30-OCT-2000; 2000US-0243792P.
 PR 18-APR-2001; 2001US-00836353.

XX (NIJ/J) NI J.
 PA (YOUNG) YOUNG P E.
 PA (KENN) KENNY J J.
 PA (OLSE) OLSEN H S.
 PA (MOOR) MOORE P A.
 PA (WEI) WEI Y.
 PA (GREEN) GREENE J M.
 PA (RUBEN) RUBEN S M.
 PA (LIU) LIU D.
 PA (CROCK) CROCKER P R.
 XX
 PI NI J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
 PI Ruben SM, Liu D, Crocker PR;
 PI WPI: 2003-567103/53.
 DR

PT New human secreted nucleic acid molecules and polypeptides, useful for
 PT preventing, treating, or ameliorating a medical condition, such as
 PT cancer, inflammation, immune disorders, neurological and blood clotting
 PT disorders.

PS Disclosure; Page 72; 454p; English.

XX The invention relates to an isolated nucleic molecule that is at least
 CC 95% identical to 18 human cDNA sequences representing 12 novel genes
 CC encoding secreted proteins or a polynucleotide fragment of the cDNA
 CC sequence contained in American Type Culture Collection (ATCC) deposit No.
 CC defined in the specification, its species homologue, a variant or allelic
 CC variant of the polynucleotide having a polynucleotide capable of
 CC hybridizing under stringent conditions to a nucleic acid molecule
 CC does not hybridize under stringent conditions to a nucleic acid molecule
 CC having a nucleotide sequence of only A or T residues. Also included are
 CC recombinant vectors, host cells (for producing the polypeptide), the
 CC secreted polypeptide (comprising a sequence that is at least 95%
 CC identical to a polypeptide fragment, domain, epitope, full-length
 CC protein, variant, allelic variant or species homologue), antibodies that
 CC specifically bind to the polypeptides, diagnosing, treating, preventing
 CC or ameliorating a medical condition by administering the polynucleotide
 CC or the polypeptide, the gene corresponding to the cDNA sequence and
 CC identifying an activity in a biological assay (by expressing the cDNA
 CC sequence in a cell, isolating the supernatant, and detecting an activity
 CC in a biological assay and identifying the protein in the supernatant
 CC having the activity). The polypeptides, nucleic acids and antibodies are
 CC useful for diagnosing a pathological condition or a susceptibility to a
 CC pathological condition, for preventing, treating, or ameliorating a
 CC medical condition, such as cancer, inflammation and other immune
 CC disorders, neurological and blood clotting disorders (many examples are
 CC given in the specification). The nucleic acids are also useful for
 CC chromosome identification, radiation hybrid mapping or long-range
 CC restriction mapping. The polypeptides and antibodies are useful for
 CC providing immunological probes for differential identification of the
 CC tissues immunohistochemistry assays. The polypeptide, polynucleotide,
 CC agonist or antagonist may also be used as a food additive or preservative
 CC to increase or decrease storage capabilities, fat content or other
 CC nutritional components. The present is a secreted protein of the
 CC invention.

XX Sequence 442 AA:

Query Match 98.7%; Score 2169; DB 6; Length 442;
 Best Local Similarity 98.8%; Pred. No. 2.1e-149;
 Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGRLRLRLLLLSAALIPFGDGNLFKQDVTVEGEVATISGVNKSDDSVIQLN 60
 DB 19 AAPGRLRLRLLLLSAALIPFGDGNLFKQDVTVEGEVATISGVNKSDDSVIQLN 78
 QY 61 PNRQTIYFRDPRPLKDSRFQNLNFSSELKSLTNVISDEGRYFCQLYTDPQESYTTI 120
 DB 79 PNRQTIYFRDPRPLKDSRFQNLNFSSELKSLTNVISDEGRYFCQLYTDPQESYTTI 138
 QY 121 TLVPPRNLMIDIQKQTAVEGEIEVNCTAMASKPATTTIRFKGNTELKGSVEEWSDM 180

XX 10-JUL-2003.
 PD XX
 PF 18-APR-2001; 2001US-00836353.
 XX
 PR 28-OCT-1998; 98US-0105971P.
 PR 27-OCT-1999; 99WO-US025031.
 PR 19-APR-2000; 2000US-0198407P.
 XX
 PA (NITJ/) NI J.
 PA (YOUN/) YOUNG P E.
 PA (KENN/) KENN J J.
 PA (OLSE/) OLSEN H S.
 PA (MOOR/) MOORE P A.
 PA (WEIY/) WEI Y.
 PA (GREEN/) GREENE J M.
 PA (RUBE/) RUBEN S M.
 XX
 PI Ni J, Young PE, Kenny JU, Olsen HS, Moore PA, Wei Y, Greene CM;
 PI Ruben SM;
 XX
 DR WPI; 2004-020335/02.
 XX
 PT New nucleic acid molecule, useful for preparing a medicament for
 PT preventing, treating or ameliorating a medical condition e.g. cancer,
 PT liver disorders or neural disorders.
 XX
 PS Disclosure; SEQ ID NO 136; 380bp; English.
 XX
 CC The invention relates to an isolated nucleic acid sequence, or its
 CC allelic variant, a fragment of the cDNA sequence, or its fragment,
 CC domain, epitope or species homologue. The nucleic acid is useful for
 CC preparing a medicament for preventing, treating or ameliorating a medical
 CC condition e.g., cancer, liver disorders such as hepatitis or neural
 CC disorders such as Alzheimer's disease. The present sequence represents
 CC the amino acid sequence of a novel human secreted protein associated
 CC protein.
 CC
 XX
 SQ Sequence 442 AA;
 Query Match 98.7%; Score 2169; DB 8; Length 442;
 Best Local Similarity 98.8%; Pred. No. 2,1e-149;
 Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

DB 439 EYF 441
 |||
 RESULT 10
 ABO07196
 ID ABO07196 standard; protein; 442 AA.
 XX
 AC ABO07196;
 XX
 DT 13-AUG-2003 (first entry)
 XX
 DE Human p53 modifying protein, SEQ ID 156.
 XX
 KW Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
 KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
 KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
 KW apoptotic disorder; cell proliferation disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200299122-A1.
 XX
 PD 12-DEC-2002.
 XX
 PF 03-JUN-2002; 2002WO-US017382.
 XX
 PR 05-JUN-2001; 2001US-0296076P.
 PR 10-OCT-2001; 2001US-0328605P.
 PR 15-FEB-2002; 2002US-0357253P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Friedman L, Plozman GD, Belvin M, Francis-Liang H, Li D, Funke RP;
 XX
 DR WPI; 2003-156859/15.
 DR
 XX N-PSDB; ACD13371.
 XX
 PT Identifying modulators of the p53 pathway for use in treating apoptotic
 PT or cell proliferation disorders, comprises screening for agents that
 PT modulate activity of a human ortholog of genes that modify the p53
 PT pathway in Drosophila.
 XX
 PS Example 2; Page 469-470; 678bp; English.
 XX
 CC The invention relates to identifying (M1) a candidate p53 pathway
 CC modulating agent, by contacting an assay system comprising a purified HM
 CC polypeptide (human orthologue of genes that modify the p53 pathway in
 CC Drosophila) or nucleic acid with a test agent under conditions, where but
 CC for the presence of the test agent, the system provides a reference
 CC activity, and detecting a test agent-biased activity of the assay system.
 CC Also included are modulating (M2) a p53 pathway of a cell (comprising
 CC contacting a cell defective in p53 function with a candidate modulator
 CC that specifically binds to a HM polypeptide comprising an HM amino acid
 CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
 CC in a mammalian cell (comprising contacting the cell with an agent that
 CC specifically binds an HM polypeptide or nucleic acid), and diagnosing (M4)
 CC a disease in a patient (comprising: (a) obtaining a biological sample
 CC from the patient; (b) contacting the sample with a probe for HM
 CC expression; (c) comparing the results with a control; and (d) determining
 CC whether the comparison indicates a likelihood disease). (M1) is useful
 CC for identifying modulators of the p53 pathway. A probe for HM expression
 CC in a patient, where the cancer has greater than 25 % expression level.
 CC Modulators identified by (M1) are useful in a variety of diagnostic and
 CC therapeutic applications, where disease or disorder prognosis is related
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
 CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
 CC the p53 function of the cell, so that the cell undergoes normal
 CC proliferation or progression through the cell cycle. (M2) and (M3) are
 CC also useful for treating defects in the p53 pathway such as angiogenic,
 CC apoptotic or cell proliferation disorders. The present sequence

CC	represents a human p53 pathway modifying protein					
XX	Sequence 442 AA;					
	Query Match	98.6%;	Score 2166;	DB 6;	Length 442;	
	Best Local Similarity	98.6%;	Pred. No. 3.4e-149;			
	Matches 417; Conservative	2;	Mismatches 4;	Indels 0;	Gaps 0	
QY	1 AAPPGRRLRLILLLSAALIFPTGGQNLFITDVIIVIGEVATISCVNKSDDSVIQLLN 60					
Dd	19 AAPPGRLRLILLLSFAALIFTGQGNIETYDVIVIGEVATISCVNKSDDSVIQLLN 78					
QY	61 PNRQTIFYRDFRLKDSRFQLNFSSSELKVSILTVWSISDEGRYCQLHTDPQESYTTI 120					
Dd	79 PNRQTIFYRDFRLKDSRFQLNFSSSELKVSILTVWSISDEGRYCQLHTDPQESYTTI 138					
QY	121 TVLVPPRNLMIDIQKTAVEGEIEVNCVTAMASKPATITIRPFKNKEIKSKSEVEWSDM 180					
Dd	139 TVLVPPRNLMIDIQRDTAVEGEIEVNCVTAMASKPATITIRPFKNKEIKSKSEVEWSDM 198					
QY	181 YTVTSQMLKVHNEGDGVPICOVEHPATVNTLTOTRELYOXYPOVAHQWTPELQGLTR 240					
Dd	199 YTVTSQMLKVHNEGDGVPICOVEHPATVNLQTORLEVOYQOVHIQMTPLQGLTR 258					
QY	241 EGDAPFELTCAIGKPQPVMTWVRVDENDEPQHAVLSGENLEINNINKTDNGYCEASNI 300					
Dd	259 EGDALETTCAGIKGPQPVMTWVRVDENDEPQHAVLSGENLFINLNKTDNGYCEASNI 318					
QY	301 VGRASHDYMLXVYDPTTIPRPPTTTTTTTTTTTTTLLIIITDSRAGEGTIGAVDAVIG 360					
Dd	319 VGRASHDYMLXVYDPTTIPRPPTTTTTTTTTTTTTLLIIITDSRAGEGSLRAVDHAVIG 378					
QY	361 GVVAVVVFAMLCLIIILGRYFARHKGYTFTHAKGADPADADPAIINAEGGQNNSEKK 420					
Dd	379 GVVAVVVFAMLCLIIILGRYFARHKGYTFTHAKGADPADADPAIINAEGGQNNSEKK 438					
QY	421 EYF 423					
Dd	439 EYF 441					
 RESULT 11 ABO07231						
ID	ABO07231 standard; protein; 442 AA.					
XX	AC					
XX	ABO07231;					
XX	DT					
XX	13-AUG-2003 (first entry)					
Dd	Human p53 modifying protein, SEQ ID 191.					
XX	Human; p53 modifier; cytosolic; cancer; cytosolic; antiangiogenic;					
KW	antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;					
KW	lung cancer; ovarian cancer; angiogenesis; cell cycle;					
XX	apoptotic disorder; cell proliferation disorder.					
OS	Homo sapiens.					
XX	WO200299122-A1.					
PN	12-DEC-2002.					
PD	03-JUN-2002; 2002MO-US017382.					
PF	05-JUN-2001; 2001US-0296076P.					
XX	PR 10-OCT-2001; 2001US-0328605P.					
XX	PR 15-FEB-2002; 2002US-0357253P.					
XX	(EXEL-) EXELIXIS INC.					
FI	Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP,					
WR	WPJ; 2003-156859/15.					

Query Match	98.6%	Score 2166	DB 6	Length 442
Best Local Similarity	98.6%	Pred. No. 3.4e-149		
Matches 417	Conservative	2	Mismatches 4	Indels 0
			Gaps	0
Query	1	AAPGGLRLRLTLTLTSAALPTGDSGNLPRKDVTEGEVATISCCVYKNSDDSVYQLLN	60	
Ds	19	AAPGGLRLRLTLTLTSAALPTGDSGNLPRKDVTEGEVATISCCVYKNSDDSVYQLLN	78	
QY	61	ENRQTIYFRDERPLKDSRFQILNFSSESLKVLTVNSISDEGRYFCQYLTDPQDSYTTI	120	
Ds	79	PNRQTIYFRDERPLKDSRFQILNFSSESLKVLTVNSISDEGRYFCQYLTDPQDSYTTI	138	
QY	121	TVLVPENINIMDICKDAVESEELVNVCTAASKPATIIRFKNGKELKGSVEWESDM	180	
Ds	139	TVLVPENINIMDICKDAVESEELVNVCTAASKPATIIRFKNGKELKGSVEWESDM	198	
QY	181	YTVTSQMLKVKHEDDGVPIVQVEHFAVNTLQTORYLEVQYKRVHIIQWTPPLQGLTR	240	
Ds	199	YTVTSQMLKVKHEDDGVPIVQVEHFAVNTLQTORYLEVQYKRVHIIQWTPPLQGLTR	258	
QY	241	EGDAFELTCEALIGRPQVMTWTVSVDDEMPHVALSGNLFINNLTKNQDNGTYRCEASNI	300	
Ds	259	EGDAFELTCEALIGRPQVMTWTVSVDDEMPHVALSGNLFINNLTKNQDNGTYRCEASNI	318	
QY	301	VGKAHSDYMLVYVDPPTIIPPTITTTTTTTTTTTTTTTTTTTTTTDSRAGEGIIIGAVDHAIVG	360	
Ds	319	VGKAHSDYMLVYVDPPTIIPPTITTTTTTTTTTTTTTTTTTTTTTDSRAGEGIIIGAVDHAIVG	378	
QY	361	GVAVVVFVFMCLIIIGRYFAHKGTYFTHEAGGADDAADAPRAIINAEQGNNSSEKK	420	
Ds	379	GVAVVVFVFMCLIIIGRYFAHKGTYFTHEAGGADDAADAPRAIINAEQGNNSSEKK	438	

QY 421 EYF 423
|||
Db 439 EYF 441

RESULT 12
ADE61605
ID ADE61605 standard; protein: 442 AA.
AC ADE61605;
XX
XX
DT 29-JAN-2004 (first entry)
XX
XX Human Protein AAF69029, SEQ ID NO 7525.
DE
XX Human pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
OS Homo sapiens.
XX
XX MO2003016475-A2.
PN
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002MO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GHEO) GEN HOSPITAL CORP.
FA (FARB) BAYER AG.
XX
XX Woolf C, D'Urso D, Befort K, Costigan M;
PI WPI: 2003-266312/26.
DR GENBANK; AAF69029.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page: 1017P; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 442 AA:

Query Match 98.6%; Score 2166; DB 7; Length 442;
Best Local Similarity 98.6%; Pred. No. 3,4e-149;
Matches 417; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLILLLLSAAALIPFGDGNLTFTKVTVEGVAITISQVKNKSDSVIQLLN 60
Db 19 AAPPGLRLRLILLLLSAAALIPFGDGNLTFTKVTVEGVAITISQVKNKSDSVIQLLN 78
QY 61 ENROTIYFRDPRLPKDSRFOLLNFSSELSKSLTNVSISEGRYFCQLYTDPQESYTTI 120
Db 79 ENROTIYFRDPRLPKDSRFOLLNFSSELSKSLTNVSISEGRYFCQLYTDPQESYTTI 138
QY 121 TLVPPRNLMIDIGKDTAVBGEIEIVNCTMASKPATTTIMFGKNELKCKSEVEKSDM 180
Db 139 TLVPPRNLMIDIGKDTAVBGEIEIVNCTMASKPATTTIMFGKNELKCKSEVEKSDM 198
QY 181 YTVTSQMLKVKHKEDDGPVYICQVEHPAVTGNLQYRILEVQYKPOVHIQMTYPLQGLTR 240
Db 199 YTVTSQMLKVKHKEDDGPVYICQVEHPAVTGNLQYRILEVQYKPOVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIGKRPQVMTWVRVDDEMPQHAVLSGPNLFINLNKXTDNGTACEASNI 300
Db 259 EGDALFELTCEAIGKRPQVMTWVRVDDEMPQHAVLSGPNLFINLNKXTDNGTACEASNI 318
QY 301 VGKASDYMLYVVPPTTTPPTTTTTLTTLTITDSRAGEEGTIGAVDAVIG 360
Db 319 VGKASDYMLYVVPPTTTPPTTTTTLTTLTITDSRAGEEGTIGAVDAVIG 378
QY 361 GVNAVVFVAMLCIIIGRYFARHKGTFTHEAKGADDAADATAIINAEQGNSEKK 420
Db 379 GVNAVVFVAMLCIIIGRYFARHKGTFTHEAKGADDAADATAIINAEQGNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

RESULT 13
ADE61608
ID ADE61608 standard; protein: 442 AA.
XX
XX ADE61608;
XX
XX 29-JAN-2004 (first entry)
DT
XX
XX Human Protein AAF69029, SEQ ID NO 7528.
DE
XX
XX Human pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
OS
XX
XX WO2003016475-A2.
PN
XX
PD 27-FEB-2003.
XX
XX 14-AUG-2002; 2002MO-US025765.
PF
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'Urso D, Befort K, Costigan M;
PI WPI: 2003-266312/26.
DR GENBANK; AAF69029.
XX
XX New composition comprising two or more isolated polypeptides, useful for

QY 181 YTVTSQMLKVKHKEDDGVPIICQVEHPATVGNLQOTQRYLEVOYKPOVHIOMTYPRQGLTR 240
 Db 197 YTVTSQMLKVKHKEDDGVPIICQVEHPATVGNLQOTQRYLEVOYKPOVHIOMTYPRQGLTR 256
 QY 241 EGDAPFELTCEAIGKPGQPVMTWVRVDEMPQHAVLSGPNLFINNKTDNGTYRCEASNI 300
 Db 257 EGDALFELTCEAIGKPGQPVMTWVRVDEMPQHAVLSGPNLFINNKTDNGTYRCEASNI 316
 QY 301 VGKASDVMKYVYDPPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTGAVDHAVIG 360
 Db 317 VGKASDVMKYVYDPPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTGAVDHAVIG 376
 QY 361 GVAVVVFMFLCILLIGRYFARHKGTFTYTHAKGADDAADTAIINAEGGQNNSEKK 420
 Db 377 GVAVVVFMFLCILLIGRYFARHKGTFTYTHAKGADDAADTAIINAEGGQNNSEKK 436
 QY 421 EYF 423
 Db 437 EYF 439

RESULT 15

AAB01321
 ID AAB01321 standard; protein; 440 AA.

AC AAB01321;

DT 25-SEP-2000 (first entry)

DE Human PRO355 polypeptide.

XX PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243;
 KW PRO745; PRO341; PRO323; PRO299; PRO333; PRO344; PRO347; PRO355; PRO353;
 KM PRO361; PRO365; transmembrane polypeptide; antibody; screening;
 KW detection; inhibition; probe; primer; human.
 XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

FT Modified-site 427..433
 FT /note= "N-myristoylation site"
 FT Modified-site 428..432
 FT /note= "N-myristoylation site"
 FT Modified-site 430..434
 FT /note= "N-glycosylation site"
 FN MO200032776-A2.

PD 08-JUN-2000.

XX 01-DEC-1999; 99NC-US026301.

XX 01-DEC-1998; 98WC-US025108.

PR 16-DEC-1998; 98US-0112850P.

PR 22-DEC-1998; 98US-0113296P.

XX (GETH) GENENTECH INC.

XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E,
 PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL,
 PI Hillan KJ, Kijavlin ID, Napier WA, Roy WA, Tumas D, Wood WI;

DR WPI: 2000-412324/35.

XX N-PSDB: AAA49563.

FT New human nucleic acids encoding secreted and transmembrane polypeptides,
 FT designated as PRO polypeptides, useful as pharmaceutical and diagnostic
 PT agents.

XX Claim 12; Fig 24; 187pp; English.

XX New human nucleic acids encoding secreted and transmembrane polypeptides
 CC which are designated as PRO polypeptides are described. The membrane-bound
 CC proteins have various industrial applications, including as
 CC pharmaceutical and diagnostic agents. The membrane-bound proteins can
 CC also be employed for screening of potential peptide or small molecule
 CC inhibitors of the relevant receptor/ligand interaction. Anti-PRO
 CC antibodies are useful for the affinity purification of PRO from
 CC recombinant cell culture or natural sources
 CC

XX Sequence 440 AA;

Query Match 97.8%; Score 2149; DB 3; Length 440;
 Best Local Similarity 98.3%; Pred. No. 5.8e-148;
 Matches 416; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 1 AAPPGLRLILLLSAAALIPFGDGNLFTKVTYIEGVATISQVNSDSDSVIQLN 60

Db 19 AAPPG--LRILLLFSAALIPFGDGNLFTKVTYIEGVATISQVNSDSDSVIQLN 76

QY 61 PNRQTIYFRDPRPKDSRFOQLNFSSELKVSITNVSISDEGRYFCQLYTDPQESYTTI 120

Db 77 PNRQTIYFRDPRPKDSRFOQLNFSSELKVSITNVSISDEGRYFCQLYTDPQESYTTI 136

QY 121 TVLVPPNNLMIDIOKTAVEGEELVNCITMAKSPATTIMFQNKKEIKKSEVEESDM 180

Db 137 TVLVPPNNLMIDIOKTAVEGEELVNCITMAKSPATTIMFQNKKEIKKSEVEESDM 196

QY 181 YTVTSQMLKVKHKEDDGVPIICQVEHPATVGNLQOTQRYLEVOYKPOVHIOMTYPRQGLTR 240

Db 197 YTVTSQMLKVKHKEDDGVPIICQVEHPATVGNLQOTQRYLEVOYKPOVHIOMTYPRQGLTR 256

QY 241 EGDAPFELTCEAIGKPGQPVMTWVRVDEMPQHAVLSGPNLFINNKTDNGTYRCEASNI 300

Db 257 EGDALFELTCEAIGKPGQPVMTWVRVDEMPQHAVLSGPNLFINNKTDNGTYRCEASNI 316

QY 301 VGKASDVMKYVYDPPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTGAVDHAVIG 360

Db 317 VGKASDVMKYVYDPPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTGAVDHAVIG 376

QY 361 GVAVVVFMFLCILLIGRYFARHKGTFTYTHAKGADDAADTAIINAEGGQNNSEKK 420

Db	377	GVAVVVFAMLCLLIIGRYFARHKGTFTHEAKGADDAADDTAIINABGQNNSEKK	436
Qy	421	EYF 423	
Db	437	EYF 439	

Search completed: July 7, 2004, 05:59:12
Job time : 75.3306 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 7, 2004, 06:02:51 ; Search time 606.382 Seconds

(without alignments)
217.146 Million cell updates/sec

Title: US-10-622-237-4

Perfect score: 2197
Sequence: 1 AAPGRLRLILLISAAAL.....TALINNEGONNEKKEVF 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2197	100.0	423	9	US-09-778-510-22
2	2197	100.0	423	9	US-09-778-1878-4
3	2197	100.0	423	14	US-10-302-041-22
4	2197	100.0	445	15	US-10-015-115-112
5	2176.5	99.1	494	15	US-10-015-115-113
6	2169	98.7	442	9	US-09-778-510-20
7	2169	98.7	442	9	US-09-778-1878-2
8	2169	98.7	442	10	US-09-984-130-136
9	2169	98.7	442	10	US-09-836-353A-136
10	2169	98.7	442	12	US-10-363-616-262
11	2169	98.7	442	14	US-10-302-041-20
12	2169	98.7	442	14	US-10-403-107-11
13	2169	98.7	442	15	US-10-015-115-111
14	2166	98.6	442	15	US-10-015-115-110
15	2149	97.8	440	9	US-09-866-028-61

16	2149	97.8	440	9	US-09-944-449-61	Sequence 61, App1
17	2149	97.8	440	9	US-09-944-457-61	Sequence 61, App1
18	2149	97.8	440	9	US-09-944-862-61	Sequence 61, App1
19	2149	97.8	440	9	US-09-945-587-61	Sequence 61, App1
20	2149	97.8	440	9	US-09-945-015-61	Sequence 61, App1
21	2149	97.8	440	9	US-09-944-396-61	Sequence 61, App1
22	2149	97.8	440	9	US-09-944-097-61	Sequence 61, App1
23	2149	97.8	440	9	US-09-944-432-61	Sequence 61, App1
24	2149	97.8	440	9	US-09-943-762-61	Sequence 61, App1
25	2149	97.8	440	9	US-09-944-654-61	Sequence 61, App1
26	2149	97.8	440	9	US-09-943-851A-61	Sequence 61, App1
27	2149	97.8	440	9	US-09-944-413-61	Sequence 61, App1
28	2149	97.8	440	9	US-09-944-403-61	Sequence 61, App1
29	2149	97.8	440	9	US-09-944-896-61	Sequence 61, App1
30	2149	97.8	440	9	US-09-944-944-61	Sequence 61, App1
31	2149	97.8	440	9	US-09-944-929-61	Sequence 61, App1
32	2149	97.8	440	9	US-09-944-907-61	Sequence 61, App1
33	2149	97.8	440	10	US-09-944-884-61	Sequence 61, App1
34	2149	97.8	440	10	US-09-944-852-61	Sequence 61, App1
35	2149	97.8	440	10	US-09-943-780-61	Sequence 61, App1
36	2149	97.8	440	11	US-09-945-584-61	Sequence 61, App1
37	2149	97.8	440	12	US-10-206-915-34	Sequence 34, App1
38	2149	97.8	440	12	US-10-199-670-34	Sequence 34, App1
39	2149	97.8	440	12	US-10-201-858-34	Sequence 34, App1
40	2149	97.8	440	12	US-10-205-890-34	Sequence 34, App1
41	2149	97.8	440	12	US-10-208-024-34	Sequence 34, App1
42	2149	97.8	440	12	US-10-201-853-34	Sequence 34, App1
43	2149	97.8	440	12	US-10-677-471-61	Sequence 61, App1
44	2149	97.8	440	12	US-10-677-669-61	Sequence 61, App1
45	2149	97.8	440	12	US-10-174-581-34	Sequence 34, App1

ALIGNMENTS

RESULT 1
US-09-778-510-22

Sequence 22, Application US/09778510
Patent No. US20020164686A1

GENERAL INFORMATION:
APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1

FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510

PRIOR FILING DATE: 2001-02-07
CURRENT FILING DATE: PCT/US99/17906

PRIOR APPLICATION NUMBER: 1999-08-05
PRIOR FILING DATE: 1998-08-07

NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 22

LENGTH: 423
TYPE: PRT
ORGANISM: Mus musculus

US-09-778-510-22

Query Match 100.0%; Score 2197; DB 9; Length 423;
Best Local Similarity 100.0%; Pred. No. 1,1e-170;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAPGRLRLILLISAAALITGGGOLVTFKDVTVIGEVATISCCVKNKSDSVITQLN	60
DB	1	AAPGRLRLILLISAAALITGGGOLVTFKDVTVIGEVATISCCVKNKSDSVITQLN	60
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DB	61	PKRQITVDFPPLKDSRFQNLNFSSELKSLTNVSISSDEGRYCOQYTPPOSSYTTI	120
QY	121	TVLVPPRLNMDIQDQTAVEGEIEVNCCTAMASKATTIRMFKNKELKGSVEVEWSDM	180
DB	121	TVLVPPRLNMDIQDQTAVEGEIEVNCCTAMASKATTIRMFKNKELKGSVEVEWSDM	180

QY 181 YTVTSQMLKVKHEDDGVPIQVHEPAVTGNLQTORYLEVQYKPOVHIQMTYPILOGLTR 240
DB 181 YTVTSQMLKVKHEDDGVPIQVHEPAVTGNLQTORYLEVQYKPOVHIQMTYPILOGLTR 240
QY 241 EGDFAFELTCEAIGKPOQVMTWVRVDDDEMPQHAVALSGPNLFINNLTNDGTGRCEASNI 300
DB 241 EGDFAFELTCEAIGKPOQVMTWVRVDDDEMPQHAVALSGPNLFINNLTNDGTGRCEASNI 300
QY 301 VGKASDYMUYVDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
DB 301 VGKASDYMUYVDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
QY 361 GVAAVVVFAMLCIIILIGRYFAHKGTYFTHKAGDADADADATAIINAGGQNNSEKK 420
DB 361 GVAAVVVFAMLCIIILIGRYFAHKGTYFTHKAGDADADADATAIINAGGQNNSEKK 420
QY 421 EYF 423
DB 421 EYF 423

RESULT 2
US-09-778-187B-4
; Sequence 4, Application US/09778187B
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187B
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: US 60/095,672
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: mus musculus
US-09-778-187B-4

Query Match 100.0%; Score 2197; DB 9; Length 423;
Best Local Similarity 100.0%; Pred. No. 1,1e-170;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPGRLRLULLLSAAALIPFGDQNLFTKQVTVIEGVAATISQVKNKSDSVIQLN 60
DB 1 AAPGRLRLULLLSAAALIPFGDQNLFTKQVTVIEGVAATISQVKNKSDSVIQLN 60
QY 61 PNRQTIYFRDPRPKDSRFQNLNFSSELKVSILTNVISDEGRYFCQLYTDPPOESYTTI 120
DB 61 PNRQTIYFRDPRPKDSRFQNLNFSSELKVSILTNVISDEGRYFCQLYTDPPOESYTTI 120
QY 121 TVLVPRLNLMIDIOKDTAVGESEIEVNCTAMASKPATIIRWFGNKELKXKSEVEEWSDM 180
DB 121 TVLVPRLNLMIDIOKDTAVGESEIEVNCTAMASKPATIIRWFGNKELKXKSEVEEWSDM 180
QY 181 YTVTSQMLKVKHEDDGVPIQVHEPAVTGNLQTORYLEVQYKPOVHIQMTYPILOGLTR 240
DB 181 YTVTSQMLKVKHEDDGVPIQVHEPAVTGNLQTORYLEVQYKPOVHIQMTYPILOGLTR 240
QY 241 EGDFAFELTCEAIGKPOQVMTWVRVDDDEMPQHAVALSGPNLFINNLTNDGTGRCEASNI 300
DB 241 EGDFAFELTCEAIGKPOQVMTWVRVDDDEMPQHAVALSGPNLFINNLTNDGTGRCEASNI 300
QY 301 VGKASDYMUYVDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
DB 301 VGKASDYMUYVDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
QY 361 GVAAVVVFAMLCIIILIGRYFAHKGTYFTHKAGDADADADATAIINAGGQNNSEKK 420

DB 361 GVAAVVVFAMLCIIILIGRYFAHKGTYFTHKAGDADADADATAIINAGGQNNSEKK 420
QY 421 EYF 423
DB 421 EYF 423

RESULT 3
US-10-302-041-22
; Sequence 22, Application US/10302041
; Publication No. US20030144478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/10/302,041
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-302-041-22

Query Match 100.0%; Score 2197; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 1,1e-170;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPGRLRLULLLSAAALIPFGDQNLFTKQVTVIEGVAATISQVKNKSDSVIQLN 60
DB 1 AAPGRLRLULLLSAAALIPFGDQNLFTKQVTVIEGVAATISQVKNKSDSVIQLN 60
QY 61 PNRQTIYFRDPRPKDSRFQNLNFSSELKVSILTNVISDEGRYFCQLYTDPPOESYTTI 120
DB 61 PNRQTIYFRDPRPKDSRFQNLNFSSELKVSILTNVISDEGRYFCQLYTDPPOESYTTI 120
QY 121 TVLVPRLNLMIDIOKDTAVGESEIEVNCTAMASKPATIIRWFGNKELKXKSEVEEWSDM 180
DB 121 TVLVPRLNLMIDIOKDTAVGESEIEVNCTAMASKPATIIRWFGNKELKXKSEVEEWSDM 180
QY 181 YTVTSQMLKVKHEDDGVPIQVHEPAVTGNLQTORYLEVQYKPOVHIQMTYPILOGLTR 240
DB 181 YTVTSQMLKVKHEDDGVPIQVHEPAVTGNLQTORYLEVQYKPOVHIQMTYPILOGLTR 240
QY 241 EGDFAFELTCEAIGKPOQVMTWVRVDDDEMPQHAVALSGPNLFINNLTNDGTGRCEASNI 300
DB 241 EGDFAFELTCEAIGKPOQVMTWVRVDDDEMPQHAVALSGPNLFINNLTNDGTGRCEASNI 300
QY 301 VGKASDYMUYVDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
DB 301 VGKASDYMUYVDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
QY 361 GVAAVVVFAMLCIIILIGRYFAHKGTYFTHKAGDADADADATAIINAGGQNNSEKK 420
DB 361 GVAAVVVFAMLCIIILIGRYFAHKGTYFTHKAGDADADADATAIINAGGQNNSEKK 420
QY 421 EYF 423
DB 421 EYF 423

RESULT 4
US-10-015-115-112
; Sequence 112, Application US/10015115
; Publication No. US20030207800A1

```
GENERAL INFORMATION:
APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Zernhusen, Bryan D
APPLICANT: Paturajan, Meera
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesha
APPLICANT: Gangoli, Esha A
APPLICANT: Shinkets, Richard A
APPLICANT: Taupier, Raymond J
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
FILE REFERENCE: 21402-211
CURRENT APPLICATION NUMBER: US/10/015,115
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/248,153
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: 60/249,598
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/313,283
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 205
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 112
LENGTH: 445
TYPE: PRT
ORGANISM: Mus musculus
US-10-015-115-112

Query Match      100.0%; Score 2197; DB 15; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.1e-170;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      421 EYF 423
      |||
Db      442 EYF 444

RESULT 5
US-10-015-115-113
Sequence 113, Application US/10015115
Publication No. US20030207800A1
GENERAL INFORMATION:
APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Zernhusen, Bryan D
APPLICANT: Paturajan, Meera
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesha
APPLICANT: Gangoli, Esha A
APPLICANT: Shinkets, Richard A
APPLICANT: Taupier, Raymond J
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
FILE REFERENCE: 21402-211
CURRENT APPLICATION NUMBER: US/10/015,115
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/248,153
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: 60/249,598
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/313,283
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 205
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 113
LENGTH: 494
TYPE: PRT
ORGANISM: Mus musculus
US-10-015-115-113

Query Match      99.1%; Score 2176.5; DB 15; Length 494;
Best Local Similarity 97.2%; Pred. No. 6.2e-169;
Matches 422; Conservative 1; Mismatches 0; Indels 11; Gaps 1;
```

D _b	300	EGCAFFELTCAICKPQPVVYTWVRVDEMPQHAIVLSGPRLLFINLNKNTKDNQTYGCAASNI	355
Q _y	301	VGRAHSYMYLVYVDPRPTLPPTPTTTTTTTTTTTTTLLIT-----DSRAGEG	349
D _b	360	VGRAHSYMYLVYDPRPTLPPTPTTTTTTTTTTTTTLLITDTATTEPAVHDSRAEG	419
Q _y	350	TIGAVDAVIVGVVAVVVAFMLCLIIILGRVFARHKGTYFTHBAKGADADADATAIINA	409
D _b	420	TIGAVDAVIVGVVAVVVAFMLCLIIILGRVFARHKGTYFTHBAKGADADADATAIINA	479
Q _y	410	EGGONNSEKKETV	423
D _b	480	EGGONNSEKKETV	493

RESULT 6
 US-09-778-510-20
 : Sequence 20 Application US/09778510
 : Patent No. US20020164686A1
 : GENERAL INFORMATION:
 : APPLICANT: Baum, Peter
 : TITLE OF INVENTION: Molecules Designated
 : FILE REFERENCE: 2844-US
 : CURRENT APPLICATION NUMBER: US/09/778, 510
 : CURRENT FILING DATE: 2001-02-07
 : PRIOR APPLICATION NUMBER: PCT/US99/17906
 : PRIOR FILING DATE: 1999-08-05
 : PRIOR APPLICATION NUMBER: 60/095, 663
 : PRIOR FILING DATE: 1998-08-07
 : NUMBER OF SEQ ID NOS: 22
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 20
 : LENGTH: 442
 : TYPE: PRT
 : ORGANISM: Homo sapien
 : US-09-778-510-20

Query Match	98.7%	Score 2165	DB 9	Length 442
Best Local Similarity	98.8%	Pred. No. 2.2e-168		
Matches 418; Conservative	1	Mismatches 4	Indels 0	Gaps 0

QY	1	AAPPGRLRLILLILLSAALLPTGSGQNLFTKDVTVIEGEVAATISCOVNNKSDSDVIOQLN	60
Db	19	AAPPGRLRLILLILLSAALLPTGSGQNLFTKDVTVIEGEVAATISCOVNNKSDSDVIOQLN	78
QY	61	PNKQTIYFRDFRDLKDSRFQLNLFSSSEHKSALNVSISDEGRYFCQLYTDPEQESYTTI	120
Db	79	PNKQTIYFRDFRDLKDSRFQLNLFSSSEHKSALNVSISDEGRYFCQLYTDPEQESYTTI	138
QY	121	TVLVPNRNLIMIDIQKDTAVEGEIEVNCNMAASKATIIIRPFKGNKELKGSVEEEMSDM	180
Db	139	TVLVPNRNLIMIDIQKDTAVEGEIEVNCNMAASKATIIIRPFKGNKELKGSVEEEMSDM	198
QY	181	YTVTSQMLMKVHKEDGQVPIQVHEPAVTGNLQTORILEYQYKPOVAHQMTYPLQGLTR	240
Db	199	YTVTSQMLMKVHKEDGQVPIQVHEPAVTGNLQTORILEYQYKPOVAHQMTYPLQGLTR	258
QY	241	EGDAPELTCEAIGKPOPVMTWVRVDEMPCHAVLSGNLFINNLKNTDNGTYRCEASNT	300
Db	259	EGDAPELTCEAIGKPOPVMTWVRVDEMPCHAVLSGNLFINNLKNTDNGTYRCEASNT	318
QY	301	VGSASHDMKLVYVDPPTIIPRPTTTTTTTTTTTTTLIIIDRSAGEGRTIGANDHAVIG	360
Db	319	VGSASHDMKLVYVDPPTIIPRPTTTTTTTTTTTTTLIIIDRSAGEGRTIGANDHAVIG	378
QY	361	GVVAVVVFAMLCIIILIGRYFARHKGTFTHEAKGADDAADADPAIINAEQGNNSEKK	420
Db	379	GVVAVVVFAMLCIIILIGRYFARHKGTFTHEAKGADDAADADPAIINAEQGNNSEKK	438
QY	421	EYF	423
Db	439	EYF	441

```

RESULT 7
US-09-778-187B-2
Sequence 2, Application US/09778187B
Patent No. US0020168712A1
GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Fenslow III, William C
TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
FILE REFERENCE: 2873-US
CURRENT APPLICATION NUMBER: US/09/778,187B
CURRENT FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: PCT/US99/17905
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: US 60/095,672
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 2
LENGTH: 442
TYPE: prt
ORGANISM: homo sapiens
US-09-778-187B-2

```

Query Match	98.7%	Score 2169;	DB 9;	Length 442;
Best Local Similarity	98.8%	Pred. No. 2.2e-168;		
Matches 418; Conservative	1;	Mismatches 4;	Indels 0;	Gaps 0;

Qy	1	AAPGGRRLRLILLISAAALI	PTGQGNLFTKDVI	EGEVAATIS	QVYKXSDSVI	QLLN	60
Db	19	AAPGRRLRLILLISAAALI	PTGQGNLFTKDVI	EGEVAATIS	QVYKXSDSVI	QLLN	78
Qy	61	PNRQTIYFDFRFLKDSRF	QLNIFSSSEIKVSL	INVSISDEGRYFCOL	YTDPPQESYTTI		122
Db	79	PNRQTIYFDFRFLKDSRF	QLNIFSSSEIKVSL	INVSISDEGRYFCOL	YTDPPQESYTTI		138
Qy	121	TYVYPRNIMIDIQDXTA	VEGEIEVNCANAS	KXATIIIRMFKXGKL	KGKSEVEBMSDM		180
Db	139	TYVYPRNIMIDIQDXTA	VEGEIEVNCANAS	KXATIIIRMFKXGKL	KGKSEVEBMSDM		198
Qy	181	YTVTSQMLMKVHKEDD	GVAVICQVEHP	AVTGNLQORLE	YQYKPOVHIQMTY	PLQGLTR	240
Db	199	YTVTSQMLMKVHKEDD	GVAVICQVEHP	AVTGNLQORLE	YQYKPOVHIQMTY	PLQGLTR	258
Qy	241	EGAPFELTCEAIGKPO	PVMVTVAVYDD	DEMPHAVISG	ENLITNNLKT	DNATYCEASNI	300
Db	259	EGAPFELTCEAIGKPO	PVMVTVAVYDD	DEMPHAVISG	ENLITNNLKT	DNATYCEASNI	318
Qy	301	VGRASHDNLVYVDP	PTTIPPTTTTTTTTTT	TTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTT	360
Db	319	VGRASHDNLVYVDP	PTTIPPTTTTTTTTTT	TTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTT	378
Qy	361	GVVAVVVFAMLC	LLIIIGRYFARAK	QTYFTHEAKGAD	ADADADATAI	INAEQGNNSSEKK	420
Db	379	GVVAVVVFAMLC	LLIIIGRYFARAK	QTYFTHEAKGAD	ADADADATAI	INAEQGNNSSEKK	438
Qy	421	EYF	423				
Db	439	EYF	441				

RESULT 8
 US-09-984-130-136
 : Sequence 136, Application US/09984130
 : Publication No. US20030055231A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: NI et al.
 :
 : TITLE OF INVENTION: 12 Human Secreted Protein
 :
 : FILE REFERENCE: PF489P2
 :
 : CURRENT APPLICATION NUMBER: US/09/984,130
 :
 : CURRENT FILING DATE: 2001-10-29
 :
 : PRIOR APPLICATION NUMBER: 60/243,792

```
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-130-136

Query Match      98.7%; Score 2169; DB 10; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGRLRLILLLSAALIPITGQGNLFTKDVTVIEGEVATISQVNNKSDSDSVIQLLN 60
19 AAPGRLRLILLLSAALIPITGQGNLFTKDVTVIEGEVATISQVNNKSDSDSVIQLLN 78
DB 61 PNRQTIYFRDPRPLKDSRFQOLNFSSELKVSILNVSISDEGRYFCQLYTDPPOESYTTI 120
79 PNRQTIYFRDPRPLKDSRFQOLNFSSELKVSILNVSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVLVPFRNLMTDIQKDTAVEGEIEVNCTAMASKPATIRPFKGNKELKGSVEEWSMD 180
139 TVLVPFRNLMTDIQKDTAVEGEIEVNCTAMASKPATIRPFKGNKELKGSVEEWSMD 198
DB 181 YTVTSQMLKVKHKEDDGVPIQVVEHPAVTGNLQTORYLEVQYKQVHIQMTYPIQLGTLR 240
199 YTVTSQMLKVKHKEDDGVPIQVVEHPAVTGNLQTORYLEVQYKQVHIQMTYPIQLGTLR 258
QY 241 EGDAPFELTCEALIGKQPVMTWVRVDDDEMPQHAVLSGNLFINNKNTDNGTYRCEASNI 300
259 EGDAPFELTCEALIGKQPVMTWVRVDDDEMPQHAVLSGNLFINNKNTDNGTYRCEASNI 318
DB 301 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTSDRAGEGSI 360
319 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTSDRAGEGSI 378
QY 361 GVAVVVVFAMCLLIIIGRYFARHKGYFTHEAKGADADADATAIINAEQQNNSEBK 420
379 GVAVVVVFAMCLLIIIGRYFARHKGYFTHEAKGADADADADATAIINAEQQNNSEBK 438
DB 421 EYF 423
439 EYF 441
```

```
RESULT 9
US-09-836-353A-136
; Sequence 136, Application US/09836353A
; Publication No. US20030129685A1
; GENERAL INFORMATION:
; APPLICANT: Nt et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: P4899P1
; CURRENT APPLICATION NUMBER: US/09/836,353A
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
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; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-353A-136
```

```
Query Match      98.7%; Score 2169; DB 10; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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```
QY 1 AAPGRLRLILLLSAALIPITGQGNLFTKDVTVIEGEVATISQVNNKSDSDSVIQLLN 60
19 AAPGRLRLILLLSAALIPITGQGNLFTKDVTVIEGEVATISQVNNKSDSDSVIQLLN 78
DB 61 PNRQTIYFRDPRPLKDSRFQOLNFSSELKVSILNVSISDEGRYFCQLYTDPPOESYTTI 120
79 PNRQTIYFRDPRPLKDSRFQOLNFSSELKVSILNVSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVLVPFRNLMTDIQKDTAVEGEIEVNCTAMASKPATIRPFKGNKELKGSVEEWSMD 180
139 TVLVPFRNLMTDIQKDTAVEGEIEVNCTAMASKPATIRPFKGNKELKGSVEEWSMD 198
DB 181 YTVTSQMLKVKHKEDDGVPIQVVEHPAVTGNLQTORYLEVQYKQVHIQMTYPIQLGTLR 240
199 YTVTSQMLKVKHKEDDGVPIQVVEHPAVTGNLQTORYLEVQYKQVHIQMTYPIQLGTLR 258
QY 241 EGDAPFELTCEALIGKQPVMTWVRVDDDEMPQHAVLSGNLFINNKNTDNGTYRCEASNI 300
259 EGDAPFELTCEALIGKQPVMTWVRVDDDEMPQHAVLSGNLFINNKNTDNGTYRCEASNI 318
DB 301 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTSDRAGEGSI 360
319 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTSDRAGEGSI 378
QY 361 GVAVVVVFAMCLLIIIGRYFARHKGYFTHEAKGADADADATAIINAEQQNNSEBK 420
379 GVAVVVVFAMCLLIIIGRYFARHKGYFTHEAKGADADADATAIINAEQQNNSEBK 438
DB 421 EYF 423
439 EYF 441
```

```
RESULT 10
US-10-363-616-262
; Sequence 262, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 262
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-262
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Query Match      98.7%; Score 2169; DB 12; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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```
QY 1 AAPGRLRLILLLSAALIPITGQGNLFTKDVTVIEGEVATISQVNNKSDSDSVIQLLN 60
19 AAPGRLRLILLLSAALIPITGQGNLFTKDVTVIEGEVATISQVNNKSDSDSVIQLLN 78
DB 61 PNRQTIYFRDPRPLKDSRFQOLNFSSELKVSILNVSISDEGRYFCQLYTDPPOESYTTI 120
79 PNRQTIYFRDPRPLKDSRFQOLNFSSELKVSILNVSISDEGRYFCQLYTDPPOESYTTI 138
```

QY 121 TVVPPRNLMIDIOKDTAVGEELVNCJAMASKPATTTIRFKGNELKKSSEVEEWSM 180
DB 139 TVVPPRNLMIDIOKDTAVGEELVNCJAMASKPATTTIRFKGNELKKSSEVEEWSM 198
QY 181 YTVTSQMLKVHKEDDGVPIQVHEPAVTGNLOTORYLEVOYKPOVHIOMTYPLQGLTR 240
DB 199 YTVTSQMLKVHKEDDGVPIQVHEPAVTGNLOTORYLEVOYKPOVHIOMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKPGQVMTWVRVDEMPQHAVLSGPNLFINNKTNDNGTYRCEASNI 300
DB 259 EGDALFELTCEAIGKPGQVMTWVRVDEMPQHAVLSGPNLFINNKTNDNGTYRCEASNI 318
QY 301 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
DB 319 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 378
QY 361 GVAVVVFPAMLCIIIIIGRYFAHKGTYFTHKAGDADAADADTAIINAGGONNSEKK 420
DB 379 GVAVVVFPAMLCIIIIIGRYFAHKGTYFTHKAGDADAADADTAIINAGGONNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 11

US-10-302-041-20
; Sequence 20, Application US/10302041
; Publication No. US2003014478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/10/302,041
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-302-041-20

Query Match 98.7%; Score 2169; DB 14; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.2e-168;

Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLILLSAALIPFGDGNLFTKDVTVIEGEVATISCOVNSDSDSVIQLN 60
DB 19 AAPPGLRLRLILLSAALIPFGDGNLFTKDVTVIEGEVATISCOVNSDSDSVIQLN 78
QY 61 PNRQTIYFRDPRPKDSRFQNLNFSSELKVSILNVSISDEGRYFCOLYTDPPQESYTTI 120
DB 79 PNRQTIYFRDPRPKDSRFQNLNFSSELKVSILNVSISDEGRYFCOLYTDPPQESYTTI 138
QY 121 TVVPPRNLMIDIOKDTAVGEELVNCJAMASKPATTTIRFKGNELKKSSEVEEWSM 180
DB 139 TVVPPRNLMIDIOKDTAVGEELVNCJAMASKPATTTIRFKGNELKKSSEVEEWSM 198
QY 181 YTVTSQMLKVHKEDDGVPIQVHEPAVTGNLOTORYLEVOYKPOVHIOMTYPLQGLTR 240
DB 199 YTVTSQMLKVHKEDDGVPIQVHEPAVTGNLOTORYLEVOYKPOVHIOMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKPGQVMTWVRVDEMPQHAVLSGPNLFINNKTNDNGTYRCEASNI 300
DB 259 EGDALFELTCEAIGKPGQVMTWVRVDEMPQHAVLSGPNLFINNKTNDNGTYRCEASNI 318

QY 301 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
DB 319 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 378
QY 361 GVAVVVFPAMLCIIIIIGRYFAHKGTYFTHKAGDADAADADTAIINAGGONNSEKK 420
DB 379 GVAVVVFPAMLCIIIIIGRYFAHKGTYFTHKAGDADAADADTAIINAGGONNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 12

US-10-403-107-1
; Sequence 1, Application US/10403107
; Publication No. US20030165974A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHU1770-1
; CURRENT APPLICATION NUMBER: US/10/403,107
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/930,803
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-107-1

Query Match 98.7%; Score 2169; DB 14; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.2e-168;

Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLILLSAALIPFGDGNLFTKDVTVIEGEVATISCOVNSDSDSVIQLN 60
DB 19 AAPPGLRLRLILLSAALIPFGDGNLFTKDVTVIEGEVATISCOVNSDSDSVIQLN 78
QY 61 PNRQTIYFRDPRPKDSRFQNLNFSSELKVSILNVSISDEGRYFCOLYTDPPQESYTTI 120
DB 79 PNRQTIYFRDPRPKDSRFQNLNFSSELKVSILNVSISDEGRYFCOLYTDPPQESYTTI 138
QY 121 TVVPPRNLMIDIOKDTAVGEELVNCJAMASKPATTTIRFKGNELKKSSEVEEWSM 180
DB 139 TVVPPRNLMIDIOKDTAVGEELVNCJAMASKPATTTIRFKGNELKKSSEVEEWSM 198
QY 181 YTVTSQMLKVHKEDDGVPIQVHEPAVTGNLOTORYLEVOYKPOVHIOMTYPLQGLTR 240
DB 199 YTVTSQMLKVHKEDDGVPIQVHEPAVTGNLOTORYLEVOYKPOVHIOMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKPGQVMTWVRVDEMPQHAVLSGPNLFINNKTNDNGTYRCEASNI 300
DB 259 EGDALFELTCEAIGKPGQVMTWVRVDEMPQHAVLSGPNLFINNKTNDNGTYRCEASNI 318
QY 301 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
DB 319 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 378
QY 361 GVAVVVFPAMLCIIIIIGRYFAHKGTYFTHKAGDADAADADTAIINAGGONNSEKK 420
DB 379 GVAVVVFPAMLCIIIIIGRYFAHKGTYFTHKAGDADAADADTAIINAGGONNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 13

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US-10-015-115-111
; Sequence 111, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Patnrajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangoli, Esna A
; APPLICANT: Shinkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILS REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 111
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-111

Query Match          98.7%; Score 2169; DB 15; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLLLLSAALLIPTGQNLFTKQVTVIEGVATTSCQVNSDSDSVIQLN 60
DB 19 AAPPGLRLRLLLLSAALLIPTGQNLFTKQVTVIEGVATTSCQVNSDSDSVIQLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILTNVSIISDEGRYFCQLYTPPOESYTTI 120
DB 79 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILTNVSIISDEGRYFCQLYTPPOESYTTI 138
QY 121 TVLVPFRNLIMIDIOKQTAVEGEIEIVNCTAMASKPATIRPFKGNELKKSSEVEWSDM 180
DB 139 TVLVPFRNLIMIDIOKQTAVEGEIEIVNCTAMASKPATIRPFKGNELKKSSEVEWSDM 198
QY 181 YTVTSQMLKVKHKEDDGPVLCQVEHPAVTGNLTQGRYLEVOYKQVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHKEDDGPVLCQVEHPAVTGNLTQGRYLEVOYKQVHIQMTYPLQGLTR 258
QY 241 EGDGFELTCEAIGFQVMTWVAVVDEMPQHNLSPNLFNNKNTDNGTGRCEASNI 300
DB 259 EGDGFELTCEAIGFQVMTWVAVVDEMPQHNLSPNLFNNKNTDNGTGRCEASNI 318
QY 301 VGKASDYMALVYDPPFTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
DB 319 VGKASDYMALVYDPPFTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378

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QY 361 GVAVAVFAMLCLLIILGRYFARHKGTYFTHAKGADDAADATAIINAEGGQNNSEKK 420
DB 379 GVAVAVFAMLCLLIILGRYFARHKGTYFTHAKGADDAADATAIINAEGGQNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 14
US-10-015-115-110
; Sequence 110, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Patnrajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangoli, Esna A
; APPLICANT: Shinkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILS REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 110
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-110

Query Match          98.6%; Score 2166; DB 15; Length 442;
Best Local Similarity 98.6%; Pred. No. 3.9e-168;
Matches 417; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLLLLSAALLIPTGQNLFTKQVTVIEGVATTSCQVNSDSDSVIQLN 60
DB 19 AAPPGLRLRLLLLSAALLIPTGQNLFTKQVTVIEGVATTSCQVNSDSDSVIQLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILTNVSIISDEGRYFCQLYTPPOESYTTI 120
DB 79 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILTNVSIISDEGRYFCQLYTPPOESYTTI 138
QY 121 TVLVPFRNLIMIDIOKQTAVEGEIEIVNCTAMASKPATIRPFKGNELKKSSEVEWSDM 180
DB 139 TVLVPFRNLIMIDIOKQTAVEGEIEIVNCTAMASKPATIRPFKGNELKKSSEVEWSDM 198
QY 181 YTVTSQMLKVKHKEDDGPVLCQVEHPAVTGNLTQGRYLEVOYKQVHIQMTYPLQGLTR 240

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Db 199 YTVISQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTR 258
QY 241 EGDAPFLTCEAIGKPOVMTWVRVDDMPQHAVLGSEPNLFINNLKNTDNGTYRCEASNI 300
Db 259 EGDALLETCEAIGKPOVMTWVRVDDMPQHAVLGSEPNLFINNLKNTDNGTYRCEASNI 318
QY 301 VGKASDYMVLVYDPPPTTITTT 360
Db 319 VGKASDYMVLVYDPPPTTITTT 378
QY 361 GVAVVVFAMLCIIIIIGRYFARHKGTFTHEAKGADDAADADTAIINAEQGQNNSEKK 420
Db 379 GVAVVVFAMLCIIIIIGRYFARHKGTFTHEAKGADDAADADTAIINAEQGQNNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

RESULT 15

US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

Query Match 97.8%; Score 2149; DB 9; Length 440;

Best Local Similarity 98.3%; Pred. No. 9.3e-167;
Matches 416; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 1 AAPPGLRLRLILLLLSAALIFPTGDQNLFTKDYTVIEGEVATISQVKNKSDSDSVTQLIN 60
Db 19 AAPPG-LRLLLLFSAALIFPTGDQNLFTKDYTVIEGEVATISQVKNKSDSDSVTQLIN 76
QY 61 PNRQTIYFRDFRPLKDSRFQLNFSSELSKSLTNVSISEGRYFCQLYTDPPQESYTTI 120
Db 77 PNRQTIYFRDFRPLKDSRFQLNFSSELSKSLTNVSISEGRYFCQLYTDPPQESYTTI 136
QY 121 TVLVPPRNLMIDIQKTAVEGEIEVNTAMASKPATTTIRWFKGNKELKGKSEVEBWSDM 180
Db 137 TVLVPPRNLMIDIQKTAVEGEIEVNTAMASKPATTTIRWFKGNKELKGKSEVEBWSDM 196
QY 181 YTVISQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTR 240
Db 197 YTVISQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTR 256

QY 241 EGDAPFLTCEAIGKPOVMTWVRVDDMPQHAVLGSEPNLFINNLKNTDNGTYRCEASNI 300
Db 257 EGDALLETCEAIGKPOVMTWVRVDDMPQHAVLGSEPNLFINNLKNTDNGTYRCEASNI 316
QY 301 VGKASDYMVLVYDPPPTTITTT 360
Db 317 VGKASDYMVLVYDPPPTTITTT 376
QY 361 GVAVVVFAMLCIIIIIGRYFARHKGTFTHEAKGADDAADADTAIINAEQGQNNSEKK 420
Db 377 GVAVVVFAMLCIIIIIGRYFARHKGTFTHEAKGADDAADADTAIINAEQGQNNSEKK 436
QY 421 EYF 423
Db 437 EYF 439

Search completed: July 7, 2004, 06:39:09
Job time : 607.382 secs

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